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Sequence 44,
Sequence 44,
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1 MEPNGTFSNNNSRNCTIENF.......KAKTKCVFPVSVWLRKETRV 330
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Sequence 44,
Sequence 2,
Sequence 182
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Sequence 30,
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Sequence 8,
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Sequence 7
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(cgn2_bfcodata/1/iaa/5A_COMB.pep:*
(cgn2_bfcodata/1/iaa/5B_COMB.pep:*
(cgn2_bfcodata/1/iaa/6A_COMB.pep:*
(cgn2_bfcodata/1/iaa/6B_COMB.pep:*
(cgn2_bfcodata/1/iaa/BCTUS_COMB.pep:*
(cgn2_bfcodata/1/iaa/BCTUS_COMB.pep:*
(cgn2_bfcodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-04-404A-2
US-09-04-404A-2
US-09-086-924-44
US-09-29-843A-44
US-09-088-337B-44
US-09-109-133-44
PCT-US93-11153-44
PCT-US95-07180-2
US-08-13-9748-374
US-08-17-95D-182
US-08-17-95D-182
US-08-17-95D-184
US-08-58-58-44
US-08-38-58-44
US-08-38-58-44
US-08-38-58-44
US-08-38-98-78-44
US-09-99-98-98-98-44
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US-08-467-948A-30
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Maximum Match 100%
Listing first 45 summaries
                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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442
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206, App	17, Appl	2, Appli	15, Appl	3, Appli	373, App	9, Appli	2, Appli	2, Appli	2, Appli	3, Appli	3, Appli	3, Appli	2, Appli	6, Appli	6, Appli	6, Appli	6, Appli
Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-09-170-496D-206	US-09-745-842-17	US-08-781-250-2	US-09-745-842-15	US-09-102-710B-3	US-08-513-974B-373	US-08-988-876-9	US-08-442-134A-2	US-08-444-581B-2	US-08-446-088A-2	US-08-559-524A-3	US-08-749-707-3	US-09-947-922-3	US-09-054-272-2	US-08-097-938-6	US-08-476-000-6	US-08-472-840-6	US-08-476-976-6
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361	377	370	374	374	373	342	375	375	375	375	375	375	342	398	398	398	398
25.4	25.4	25.1	24.8	24.5	24.3	24.3	24.3	24.3	24.3	24.3	24.3	24.3	23.9	23.7	23.7	23.7	23.7
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                            APPLICANT: Gluckemann, Maria Alexandra
APPLICANT: Gluckemann, Maria Alexandra
APPLICANT: Gluckemann, Maria Alexandra
TITLE OF INVENTION: 43239, A No. 6586205el GPCR-Like Molecule and
TITLE OF INVENTION: Uses Thereof
TITLE OF INVENTION: Uses Thereof
TITLE OF INVENTION: Uses Thereof
CURRENT APPLICATION UNMBER: US/09/585,876
CURRENT FILING DATE: 2000-66-01
EARLIER APPLICATION NUMBER: 60/182,061
EARLIER PILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
LENGTH: 346
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Sequence 2, Application US/09585876
Patent No. 6586205
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 328; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Homo sapiens
US-09-585-876-2
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Best Local Similarity
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248 PYHIQRTIHLHFLHNETKPCDSVLRMQKSVVITLSLAASNCCFDPLLYFFSGGNFRKRL- 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 LLCVCTLPLRVVYYVHKGIWLFGDFLCRLSTYALYVNLYCSIFFWTAMSFPRCIAIVFPV 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246 PYHTLRTVHLTTW--KVGLCKD--RLHKALVITLALAAANACFNPLLYYFAGENFKDRLK 301
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                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: SATHE, GANESH M.

APPLICANT: BALLSEY, WENDY

APPLICANT: ALLIS, CATHERINE E.

APPLICANT: ARES, ROBERT S.

APPLICANT: ARES, ROBERT S.

APPLICANT: CALAMBERS, JON

TITLE OF INVENTION: CDNA CLONE HMTMF81 THAT ENCODES A NOVEL

TITLE OF INVENTION: CDNA CLONE HMTMF81 THAT ENCODES A NOVEL

TITLE OF INVENTION: CDNA CLONE HMTMF81 THAT ENCODES A NOVEL

TITLE OF INVENTION: CDNA CLONE HMTMF81 THAT ENCODES A NOVEL

TITLE OF INVENTION: CDNA CLONE HMTMF81 THAT ENCODES A NOVEL

TITLE OF INVENTION: CDNA CLONE HMTMF81 THAT ENCODES A NOVEL

TITLE OF INVENTION: CDNA CLONE HMTMF81 US/09/586,924

CURRENT FILING DATE: 1998-031.9

PRIOR FILING DATE: 1998-031.9

PRIOR FILING DATE: 1998-031.9

PRIOR FILING DATE: 1997-04-22

NUMBER OF SEQ ID NOS: 2
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38.0%; Pred. No. 7.7e-36;
tive 71; Mismatches 106; Indels
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FastSEQ for Windows Version 3.0
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Patent No. 5759804
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09586924 Patent No. 6506878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 38.0%
Matches 116; Conservative
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ORGANISM: HOMO SAPIENS
                                                                      302 SALRK 306
                                                                                                                                            307 STFRK 311
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US-09-586-924-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--LQTM 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 NYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFL 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 NSRNC--TIENFKREFFFIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA CLONE HMTMF81 THAT ENCODES
A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.7%; Score 559; DB 3; Length 337; 38.0%; Pred. No. 7.7e-36;
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                                                                                            Sequence 2, Application US/09044404A

Patent No. 6200775
GENERAL INFORMATION:
APPLICANT: SATHE, GANESH
APPLICANT: HALSEY, WENDY
APPLICANT: ELIS, CATHERINE
APPLICANT: FOLEY, JAMES
APPLICANT: ARACH, HENRY
ITLE OF INVENTION: CDNB HMTMF81 THAT ENC
TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRA
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SMITHKLINE Beecham Corporation
STREET: 790 Swedeland Road, P.O. Box 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOCTWARE: FASESEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/044,404A
FILING DATE: MARCH 19, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/844,795
FILING DATE: ARRIL 22, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T.
NAME: Han, William T.
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH-70001-1
TELEDRONE: 610-270-2219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 38.0
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 790 Swedeland CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 610-270-5090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                    RESULT 2
US-09-044-404A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 HPFRLLHVTSIRSAWILCGIIWILI-MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 MNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR---KALTTIIITLIIFF 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 VCPVPYHVNRSVYVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFR 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 LCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 FSNNNSRNCTIEN-FKREFFPIVYLLIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
 No. 5759804el Seven Transmembrane Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
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Pred. No. 1.2e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62; Mismatches 126; Indels
                                                                                  STREET: 6300 Sears Tower, 233 South Wacker Drive STREET: Chicago STATE: Illinois
                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
                                                     ADDRESSEE: Marehall, O'Toole, Gerstein, Murray ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIPICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 31794
TELECOMMUNICATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRLKSAL----RKGHPQKAKTK 315
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                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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34.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 339 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 34.89
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-153-848-44
                       NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
FITLE OF INVENTION:
                                                                                                                                STATE: I
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66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMV 125
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APPLICANT: Guegler, Karl
APPLICANT: Muzong Cheng
TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.0%; Score 479; DB 2; Length 339; larity 34.8%; Pred. No. 1.2e-29; Conservative 62; Mismatches 126; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compariate
COMPUTER: IBM Compariate
SOFTWARE: FastSEQ for Windows Version 2.0
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,871
FILING APPLICATION DATA:
APPLICATION NUMBER: BILING BATE:
ATTORNS'AGENT INFORMATION:
NAME: Bilings, Lucy J
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 1D NO: 3:
SEQUENCE CHARACTERISTICS:
**PMATH: 339 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 DRLKSAL----RKGHPQKAKTK 315
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                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 992700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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Matches 112; Conserv
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RESULT 6 US-09-299-843A-44

US-08-812-871-3 ; Sequence 3, Application US/08812871 Patent No. 5955303 ; GENERAL INFORMATION:

APPLICANT: Au-Young, Janice

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 MNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR---KALTTIIITLIIFF 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              346 VCFVPYHVNRSVYVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFR 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 HPFRLLHVTSIRSAWILCGIIWILI-MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 HALVSLAVAFTFPFITTVTCYLLIIRSL-----RQGLRVEKRLKTKÄVRMIAIVLAIFL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 FSNNNSRNCTIEN-FKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Sequence 44, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
28.0%; Score 479; DB 3; Length 339;
Best Local Similarity 34.8%; Pred. No. 1.2e-29;
Matches 112; Conservative 62; Mismatches 126; Indels
                                                                                                                                                  NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                   6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGESTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMULICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-UN-1998
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 339 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                    Abb...
STREET: 65.c.
CITY: Chicago
                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-299-843A-44
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                                                                                                                                                                                                                                           APPLICANT: Godiska, Ronald
APPLICANT: Godiska, Ronald
Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: NO. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IN PC Compatible
COMPUTER: IN PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOOTWARE: Parentin Release #1.0, Version #1.25
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: -UNknown>
PRIOR APPLICATION: -UNknown>
PRIOR APPLICATION NUMBER: US 08/153,848
FILING DATA: 17-NOV-1993
FILING DATE: 17-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.0%; Score 479; DB 3; Length 33: 34.8%; Pred. No. 1.2e-29; tive 62; Mismatches 126; Indels
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-088-3378-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: NO. 6348574and, Greta E. REGISTRATION UNDRER: 35,302 REFERENCE/DOCKET UNMER: 31794 TELECOMMUNICATION INFORMATION:
298 DRLKSAL----RKGHPQKAKTK 315
                                          306 HALCNLLCGKRLKGPPPSFEGK 327
                                                                                                                                              US-09-088-337B-44; Sequence 44, Application US/09088337B; Patent No. 6348574; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ 1D NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
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Matches 112; Conservative
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STATE: Illinois
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66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMV 125
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; Pred. No. 1.2e-29;
62; Mismatches 126; Indele
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APPLICANT: GCAYNE, JEANINE D
APPLICANT: GOCAYNE, JEANINE D
APPLICANT: RUBEN, STEVEN M
TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBEB69
CORRESPONDENCE: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PATEMENT Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 07/977,452

PILING DATE: 17-NOV-1992

PILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:
NAME: NO-land, Grete E.
REGISTRATION NUMBER: 35,302

REFERNCE/DOCKET NUMBER: 31794

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 174-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
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34.8%;
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Best Local Similarity 34.8%
Matches 112; Conservative
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                                                                                             ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy
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                    CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                       FILING DATE
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APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Receptors
FILE REPERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
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192 HALVSLAVAFTFPFITTVTCYLLIIRSL-----RQGLRVEKRLKTKAVRMIAIVLAIFL 245
                                                                        66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMV 125
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APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bicknell, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US93-11153-44; Sequence 44, Application PC/TUS9311153; GENERAL INFORMATION:
                                                                                                                                            298 DRLKSAL----RKGHPQKAKTK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 DRLKSAL----RKGHPQKAKTK 315
                                                                                                                                                                                          306 HALCNLLCGKRLKGPPPSFEGK 327
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                                                                                                                                                                                                                                                                                                        Sequence 32, Application US/09170496D Patent No. 6555339 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: HOW
US-09-170-496D-32
                                                                                                                                                                                                                                                                                         -09-170-496D-32
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                                                                                                                                                                                                                                                                      7 FSNNNSRNCTIEN-FKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA
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                                                                                                                                                                       Query Match 27.8%; Score 476; DB 4; Length 339; Best Local Similarity 34.8%; Pred. No. 2e-29; Matches 112; Conservative 61; Mismatches 127; Indels
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Patent No. 6114139

GENERAL INFORMATION:
APPLICANT: Homowa, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Pujii, Ryo
APPLICANT: Pujii, Ryo
APPLICANT: Pujii, Ryo
APPLICANT: Ohdik, Tetsuya
APPLICANT: Ohdik, Razuhiro
ITILE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
ITILE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380

CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKK, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 DRLKSAL----RKGHPQKAKTK 315
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patentin version 3.1
SEQ ID NO 182
LENGTH: 339
                                                                                                 ORGANISM: Homo sapiens
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                                                                                                                          US-09-170-496D-182
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Patent No. 6555339
GRNERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Chen W.
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION INWBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 VCFVPYHVNRSVYVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKKR 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 VADLSCVLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRFLAIV 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 MNYIALVYGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR---KALTTIIITLIIFF 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 HALVSLAVAFTFPFITTVTCYLLIIRSL-----RQGLRVEKRLKTKAVRMIAIVLAIFL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMV 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 LCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 FSNNNSRNCTIEN-FKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.0%; Score 479; DB 5; Length 339; 34.8%; Pred. No. 1.2e-29; live 62; Mismatches 126; Indels
                                                                                                                                                                                         COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07180
FILING DATE: 06-JUNE-1995
                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 325800-366
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1740
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 DRLKSAL----RKGHPQKAKTK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306 HALCNLLCGKRLKGPPPSFEGK 327
ADDRESSEE: STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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US-09-170-496D-182
                                                                                            COUNTRY: U
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Sequence 14, Application US/09745842
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                                                        Conley, Pamela B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 32.18
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 NLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 AMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLL---DSGSEQNGSVTSCLE----- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTI 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRSYFVYSMCTTVFMFCI ---- PPIVILGCYGLIVKALIYKDLDNSPLR---RKSTYLV 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11TLIIFFLCFLPYHTLRTVHL-----TTWKVGLCKDRLHKALVITLALAANACFNPL 287
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252 IIVLTVPAVSYLPPHVMKTLNLRARLDFQTPQMCAFNDKVYATYQVTRGLASLNSCVDPI 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 GTPSNNNSRNCTI - - ENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFML 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81; Mismatches 114; Indels
                                                                        FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
APPLICATION NUMBER: JP 6-189272
                                                                                                                                                                                                                      FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: REGISTRATION NUMBER: 34,235
REGISTRATION NUMBER: 4575:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||: ||: ||: || || || LYFLAGDTFRRELSRATRK 330
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INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 362 amino acids
amino acid
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                  FILING DATE: 16-MAR-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: J
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Matches 98; Conserv
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RESULT 13 US-09-745-842-14

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212 RSYFIYSMCT----TVAMPC-VPLVLILGCYGLIVRALIYKDLDNSPLR---RKSIYLVI 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 IVLTVFAVSYIPPHVMKTMNLRARLDFQTPAMCAFNDRVYATYQVTRGLASLNSCVDPIL 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 LAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 MYHPFRLLHVTSIRSAWILCGIIW-ILIMASSIMLLDSGS--EQNGSVTSCLE----L 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 NLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTII 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 TPSNNNSRNC--TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.1%; Score 446; DB 4; Length 373; 32.1%; Pred. No. 4.5e-27; ive 79; Mismatches 111; Indels ;
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US-08-559-524A-4
Sequence 4, Application US/08559524A
Sequence 4, Application US/08559524A
Setent No. 5871963
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M SITEET, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: P2Y1 purinergic receptor; p2yr
APPLICANT: Gantzen, Hans-Michael
APPLICANT: Ramakrishnan-DuBridge, Vanitha
APPLICANT: Gullius, David
APPLICANT: Hollopeter, Gunter
APPLICANT: Hollopeter, Gunter
APPLICANT: COR Therapeutics, Inc.
TITLE OF INVENTION: P2712 Receptor
TITLE REFERENCE: 44481-5053-US
CURRENT APPLICATION NUMBER: US/09/745,842
CURRENT FILING DATE: 2000-12-26
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
SENGTH: 373
TYPE: PRI
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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US-08-749-707-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 PFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPFRLLHVTS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 IRSAWILCGIIWILIMASSIMLL---DSGSEQNGSVTSCLE-----LNLYKIAKLQTWN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 YIALVVGCLLPPFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIJTLIIFFLCFLP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 --TVAMFC-VPLVLILGCYGLIVRALIYKDLDNSPLR---RKSIYLVIIVLTVFAVSYIP 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YHTLRTVHL-----TTWKVGLCKDRLHKALVITLALAANACFNPLLYYFAGENFKDRL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLLFISTL
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: US/08/559,524A
FILING DATE: 15-NOV-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-08-749-707-4
iSequence 4, Application US/08749707
Fatent No. 6063582
GENERAL INFORMATION: Pamela B.
APPLICANT: Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
RESTRENCE/DOCKET NUMBER: 044481-5010-00-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: MORGAN, LEWIS & BOCKIUS LLP 1800 M Street, N.W.
PC-DOS/MS-DOS
                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                          LENGTH: 373 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington
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STREET: 18
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76 PFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPFRLLHVTS 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 IRSAWILCGIIWILIMASSIMLL---DSGSEQNGSVTSCLE-----LNLYKIAKLQTMN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 YIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFLP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 TKTGFOFYYLPAVYILVPIIGFLGNSVAİWMFVFHMKPWSGISVYMFNLALADFLYVLTL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 YHTLRIVHL-----TTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLLFISTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                    25.8%; Score ***,
31.0%; Pred. No. 9.1e-27;
rive 78; Mismatches 109; Indels
                                                                                                                                        044481-5010-01-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: August 20, 2005, 11:52:04
APPLICATION NUMBER: US/08/749,707
                                                                                          NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 0444
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEPAX: 202-467-7176
                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                   15-NOV-1996
                                                               ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
                                                                                                                                                                                                                                                                                  373 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 25.8°
Best Local Similarity 31.0°
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                   TYPE: amino acid STRANDEDNESS:
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                     FILING DATE: 15
CLASSIFICATION:
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us-09-826-7914-2 trup

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

August 20, 2005, 07:35:07 ; Search time 960 Seconds (without alignments) 176.027 Million cell updates/sec Run on:

Title: Perfect score:

US-09-826-791A-2 1712 1 MEPNGTFSNNNSRNCTIENF......KAKTKCVFPVSVWLRKETRV 330 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 Total number of hits satisfying chosen parameters:

1612378 segs, 512079187 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Lighing First 45 summaries

Uniprot f03:\*
1: uniprot sprot:\*
2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q9ns75 homo sapien	BNB	Q8r528 mus musculu	_	Q924t9 rattus norv	ratt	Q95n02 sus scrofa	-#	_	homo	Q96p68 homo sapien	rattı	homo	homo	brach		P49652 meleagris g		P34996 gallus gall	_	'n		P59902 cavia porce	Q90x57 xenopus lae		_	rattus	P47900 homo sapien	P48042 bos taurus	P49650 mus musculu	P32249 homo sapien
	QI	CLT2 HUMAN	CLT2_PIG	Q8R528	CLT2 MOUSE			CLT1_PIG	CLT1 MOUSE	CLT1 HUMAN	Q81V <u>1</u> 9	GP80_HUMAN	Q6Y1R5	GP17 HUMAN	Q8N5S7	Q7ZZA4	Q6P852	P2YR MELGA	Q61YF8	P2YR CHICK	Q6NS65	Q9DE05	068907	P2YR_CAVPO	Q90X57	Q7TMV7	P2Y5 CHICK	P2YR_RAT	P2YR_HUMAN	P2YR BOVIN	P2YR MOUSE	EBI2_HUMAN
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	Length	346	345	309	309	309	339	340	352	337	337	337	337	367	339	347	349	362	337	362	339	357	249	373	361	357	308	373	373	373	373	361
& Query	March	( 100 · O	0.65	70.3	6.69		33.1	32.9	32.7	32.7	32.3	28.5	28.0	28.0	27.9	27.9	27.7	27.5	27.3	27.3	26.8	26.7	56.6	26.5	26.5	26.3	26.1	26.1	26.1	25.8	25.8	S.
	Score	1712.	1367.5	1204	1197	1187	567.5	563	260	559	553	487.5	479	479	477	477	473.5	470	468	467	459	457	456	454	453	449.5	447	447	446	442	442	440
Result	No.	н	7	m	4	5	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

Osbmjs mus musculu	P43657 homo sapien	Q7z3s0 homo sapien	Q8bmc0 mus musculu	P41231 homo sapien	Q7z3s6 homo sapien	Q99677 homo sapien	Q6nsp5 homo sapien	Q8bkk1 mus musculu	O57466 meleagris g	P41232 rattus norv	Q8blg2 mus musculu	P35383 mus musculu	P21556 cavia porce
QBBMJS	P2YS HUMAN	072350	P2YS MOUSE	P2Y2 HUMAN	Q7Z3 <u>S</u> 6	P2Y9 HUMAN	Q6NSPS	QBBKK1	057466	P2Y2 RAT	Q8B <u>LG</u> 2	P2Y2 MOUSE	PAFR_CAVPO
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373	344	344	344	377	344	370	370	370	374	374	370	373	342
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439	437	437	436.5	434	432	430	426	425	424.5	421.5	421	418.5	416
32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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us-09-826-791a-2.rup

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330; Conservative
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TRANSMEM
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ID _CLT2_PIG
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                                                 RAY Pubbed=15057823; DOI=10.1038/nature02379;
RA Abtroff K.V., Rear D.M., Burton J., Ashurst J.L., Howe K.L.,
RA Abtroff K.J.; Beare D.M., Burton J., Andrews D.C., Hunt S.E.,
RA Griffichts-Jones S., Jones M.C., Keenan S.J., Oliver K., Scott C.E.,
RA Ainscough R., Almeida J.P., Ambrose K.D., Andrews D.T.,
RA Ainscough R., Almeida J.P., Ambrose K.D., Andrews D.T., Bannerjee R.,
RA Anscough R.F., Baselsey H., Bird C.P., Bailey J., Bannerjee R.,
RA Barlow K.F., Bares K., Basguley C.L., Bailey J., Bannerjee R.,
RA Barlow J.C., Cland M.E., Clark S.Y., Clarke G., Clee C.M.,
RA Clegg S.C., Cobley V., Collins W.C., Crorby N., Coville G.J.,
RA Clegg S.C., Cobley V., Collins J.E., Corby N., Coville G.J.,
RA Ballangton A.G., Fankland J.E., French L.,
Ranner P., Garnett J., Gilbert J., Gilbon C.J., Ghori J.,
Rally J.L., Hart E.A., Heath P.D., Howden P.J., Huckle E.J.,
Rally J.L., Hart E.A., Heath P.D., Howden P.J., Huckle E.J.,
Ring A., Laird G.K., Langford C.J., Lawlor S., Leongamornlert D.A.,
Rand W. Lloyd C., Loveland J.E., Lovell J., Martin S.,
Moore M.J.F., Nickerson T., Palmer S.A., Pearce A.V., Peck A.I.,
Rahrey J.L., Wart B.N., McLaren S.J., McMurray A., Milne S.,
Mashreghii-Mohammadi M., McLaren S.J., Mille S.,
Rehra H.K., Shownkeen B., Porter K.M., Rice C.M., Starle S.,
Rahl M., Warlis J.M., West R.P., Whitehead S.L., Willey D.L.,
Rahl M., Wallis J.M., West R.P., Whitehead S.L., Rubbard T., Sulston J.E., Bentley D.R., Rubbard T., Sulston J.E., Bentley D.R., Ruther P.D., Rature 428:522-528 (2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Homo sapiens cysteinyl leukotriene receptor 1 like receptor.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

-!-FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. Stimulation by BAY u9773, a partial agonist, induces specific contractions of pulmonary veins and might also have an indirect role in the relaxation of the pulmonary vascular endothelium. The rank order of affinities for the leukotrienes is ITC4 = ITD4 >> ITP3.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- TISSUE SPECIFICITY: Widely expressed, with highest levels in the heart, placenta, spleen, peripheral blood leukocytes and adrenal gland. In lung, expressed in the interstitial macrophages, and slightly in smooth muscle cells.

-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0004974; F:leukotriene receptor activity; NAS. GO; GO:0006955; P:immune response; NAS.
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InterPro; IPR000276; GPCR_Rhodpen.
PFfam; PF00001; 7tm 1; 1.
PRINTS; PR01533; CVSLTRECPTR.
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EMBL; AF279611; AAK69485.1;
EMBL; AB083603; BAB89316.1;
EMBL; AX389504; AAQ91330.1;
EMBL; AL137118; CAC29102.1;
EMBL; AB041644; BAB16379.1;
Genew; HGNC.18274; CYSLTR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB038269; BAB03601.1; -. EMBL; AF254664; AAG17281.1; -. EMBL; AF279611; AAK69485.1; -.
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                                      SEQUENCE FROM N.A
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61 MINIAISDILFISTIPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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( Potential).

Extracellular (Potential).

7 (Potential).

Cytoplasmic (Potential).

By similarity.

N-linked (GloNAc. . .) (Potential).

N-linked (GloNAc. . .)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
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                                                                                                      Extracellular (Potential).
1 (Potential).
Cytoplasmic (Potential).
2 (Potential).
2 (Potential).
3 (Potential).
N-linked (GlCNAc. .) (PC
N-linked (GlCNAc. .) (PC
EB54A4A2DDCESEE4 CRC64;
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Extracellular (Potential).
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28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
Name-CYSLIR2; Synonyms-CYSLIZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
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Name=Cysltr2;
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                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@18b-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLCPLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDR 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKLKTMNYVALVVGFVLPFGTLSICYLLIIRALLKVEVPESGLRLSHRKALITVIIALII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEPNGTFSNNNS-RNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Gaps
receptors.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for cysteinyl leuktrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 345;
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                                                                                                                                                                                                            Pfam; PP00001; 7tm 1; 1.
PRINTS; PR01533; CYSLTRECPTR.
PRINTS; PR00237; GPCRRHODOPSN.
PROSTITE; PS00237; GPROTEIN RECEP_F1_1; FALSE_NEG.
PROSTITE; PS050262; G PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Transmembrane.
                                                                                                                                                                                                                                                                                   Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                              Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                   Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential)
5 (Potential).
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Extracellular (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 7 (Potential).
Cytoplasmic (Potential).
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N-linked (GlcNAc. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-linked (GlcNAc. . .)
N-linked (GlcNAc. . .)
N-linked (GlcNAc. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1367.5; DB
Pred. No. 1.5e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
                                                                                                                                                                                                                                                                                                                                           (Potential).
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                                                                                                                                                                                                                                                                                              (Potential)
                                                                                                                                                                                          InterPro; IPR004071; Cysleuk_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                EMBL; AB052662; BAB60817.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39410 MW;
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79.2%;
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Best Local Similarity 79.2
Matches 262; Conservative
                                                                                                                                                                                                                                                                                              345 AA;
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241 LLCFLPYHALRTLHLVTWDKDSCGDVLHKATVITLTWAAANSCFNPFLYYFAGENFKARL 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=22013942; PubMed=11854273; DOI=10.1074/jbc.M109447200;
MEDLINE=22013942; PubMed=11854273; DOI=10.1074/jbc.M109447200;
Ogasawar H., Ishii S., Yokomizo T., Kakinuma T., Komine M.,
Tamaki K., Shimizu T., Izumi T.;
"Characterization of Mouse Cysteinyl Leukotriene Receptors mCysL71 and
mCysL72. DIFFERENTIAL PHARMACOLOGICAL PROPERTIES AND TISSUE
DISTRIBUTION.";
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 277:18763-18768 (2002).

EMBL, AB058930; BAB66881.1; -.

MGD; MG1:1917336; Cyaltr2.

GG; GO:0016021; C:integral to membrane; TAS.

GO; GO:0001631; P:cyateinyl leukotriene receptor activity; IDA.

InterPro; IPR004071; Cysleuk_receptor.

InterPro; IPR00276; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     309 AA; 35226 MW; 96FACC6B8AF96974 CRC64;
                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 70.3%; Score 1204; DB 2;
Best Local Similarity 73.4%; Pred. No. 2e-67;
Matches 226; Conservative 30; Mismatches 52;
317 LKSALRKGRPQ--KTRCGFSVCVWLKKETRV 345
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(Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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                                                                                                                                                                                                                                                                                          Cysteinyl leukotriene 2 receptor
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PRINTS; PR00237; GPCRRHODOPSN
                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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ID _CLT2_MOUSE
AC Q920A1;
DT 28-FEB-2003 (
DT 28-FEB-2003 (
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                                                                                                                                                             MEDLINE=21661669; PubMed=11591709; DOI=10.1074/jbc.M107556200;

A Uni Y., Yang G., Galczenski H., Figueroa D.J., Austin C.P.,
Copeland N.G., Gilbert D.J., Jenkins N.A., Funk C.D.;
Copeland N.G., Gilbert D.J., Jenkins N.A., Funk C.D.;
The murine cysteinyl leukotriene 2 (CysLT2) receptor. CDNA and
genomic cloning, alternative splicing, and in vitro
characterization.";
J. Biol. Chem. 276:47489-47495(2001).
L. Biol. Chem. 276:47489-47495(2001).
C. I. FUNCTION: Receptor for cysteinyl leukotrienes. The response is
mediated via a G-protein that activates a phosphatidylinositol-
calcium second messenger system. The rank order of affinities for
the leukotrienes is LTC4 = LTD4 >> LTE4.
C. INSUBCELLULAR LOCATION: Integral membrane protein.
C. ITSSUB SPECIFICITY: Widely expressed at low levels, with highest
expression in the spleen, thymus and adrenal gland, and lower in
the kidney, brain and peripheral blood leukocytes.
C. ISMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:1917336; Cysltr2.
MGD; MGI:1917336; Cysltr2.
GO; GO:0016020; C:membrane; IDA.
GO; GO:0001631; F:cysteinyl leukotriene receptor activity; IDA.
InterPro; IPR004071; Cysleuk receptor.
InterPro; IPR00276; GPCR_Rhodpsn.
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Transmembrane.
DOMAIN

Z Extracellular (Potential).
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4 (Potential).
Extracellular (Potential).
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Extracellular (Potential).
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2 (Potential).
Extracellular (Potential)
3 (Potential).
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25-OCT-2004 (Rel. 45, Last annotation update)
Cysteinyl leukotritene receptor 2 (CysLTR2).
Name-Cysltz; Synonyms-Cyslt2;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity.
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35227 MW;
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PRINTS; PR01533; CYSLTRECPTR.
PRINTS; PR00237; GPCRRHODOPSN
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                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                NCBI_TaxID=10090;
                                                                                                                                                     TISSUE=Heart;
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TRANSMEM
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SEQUENCE
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MINLAISDILFISTIPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
                          FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
                                                                                                              121 FQATVHPFRMFHVTSVRSAWILCGIIWVFIMASSALLLVNGQEEKDNIISCLELSPQKFK 180
                                                                                                                                                                          181 SLLIMNHIAVAVGFLLPFLTLTVCYLLIIRILLKAEIPESGPRAAHRKALTTIVIAMITF 240
                                                                                                                                                                                                                                241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
                                                                                                                                                                                                                                                  241 LLCFLPYHALRTLHLVTWDKDSCGDVLHKATVITLTMAAANSCFNPFLYYFAGENFKARL 300
                                                                                                                                                      181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Katasaki J., Matsumoto M., Matsumoto S., Saito T., Kambhara M., Takasaki J., Matsumoto M., Matsumoto M., Sopa T., Matsushime H., Furuichi K.; "Characterization of the cloned rat and porcine cysteinyl leukotriene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptors.", Submitted (ICC-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositoloalcium second messenger system (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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Pfam; PF00001; 7tm 1; 1.
Pfam; PRINTS; PR01533; CYSLTRECPTR.
PRINTS; PR00237; GPRCPTRIODPSN.
PROSITE; PS00237; GPROTEIN RECEP F1_1; FALSE_NEG.
PROSITE; PS0262; G PROTEIN RECEP F1_2; 1.
G-protein coupled receptor; Glycoprotein; Transmembrane.

G-protein coupled receptor; 1 (Potential).
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2 (Potential).
Extracellular (Potential).
3 (Potential).
Cytoplasmic (Potential).
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28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Cysteinyl leukotriene receptor 2 (CystirR2) (RSBPT32).
Name=Cysltr2; Synonyms=Cyslt2;
                                                                                                                                                                                                                                                                                                                                                                                                                                            309 AA
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InterPro; IPR004071; Cysleuk_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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301 RAIFSKVH 308
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61
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Gaps

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53; Indels

31; Mismatches

Matches 224; Conservative

Similarity

Local

9 9

1 MEVTGTPSSYSNRNCTIENFKKEFYPIIYLIIFFWGALGNGFSIYVFLQTCKKSTSVNVF 1 MEPNGTESNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 FPVQNINLVTQKKARFVCVGIWIFVILTSSPFLLSKSYQDEKNNTKCPEPPQDKQTKKYV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 LVLHYVSLIFGFIIPFVTIIVCYTMIILTLIKUTMKKN--LPSRRKAIGMIIVVTAAFLV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 SFMPYHIQRAIHLHFLHSETRSCDSVLRMQKSVVITLSLAASNCCFDPLLYFFSGGNFRR 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 HPFRLLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--L 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 SPSNNRCHD-TIDEFRNQVYSTMYSMISVVGFFGNSFVLYVLIKTYHEKSAFQVYMINLA 68
There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 QTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIFFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 TFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLOPYKKSTSVNVFMLNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      By similarity. (Potential)
N-linked (GlcMAc. ) (Potential)
N-linked (GlcMAc. ) (Potential)
281841DF050DF9EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 339;
                                                                                              RGD: 619796; Cysltri.

RIGERPRO; IPR004071; Cysleuk receptor.

InterPro; IPR004071; Cysleuk receptor.

InterPro; IPR00010726; GPCR_Rhodpsn.,

PRINTS; PR00133; CYSLTRECPTR.

PRINTS; PR00137; GPCRRHODOPSN.

PROSITE; PS00237; GPCRHODOPSN.

PROSITE; PS00237; GPROTEIN RECEP_F1_1; FALSE_NEG.

PROSITE; PS00237; GPROTEIN_RECEP_F1_2; I.

GPROTEIN COUPLED RECEP_F1_2; I.

GPROTEIN TRANSMEM 31 30 Extracellular (Potential).

I (POCENTIAL)
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1 (Potential).
2 (Potential).
Extracellular (Potential).
3 (Potential).
(Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential).
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Extracellular (Potential)
7 (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLKSALRK------GHPQKAKTKC 316
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28-FEB-2003 (Rel. 41, Last sequence update)
28-CCT-2004 (Rel. 45, Last annotation update)
Cysteinyl leukotriene receptor I (CysLTRI).
                                                                                                                                                                                                                                                                                                                                                                    5 (Potential).
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                                                        or send an email to license@isb-sib.ch).
 European Bioinformatics Institute.
                                                                                    EMBL; AB052685; BAB60825.1; -.
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339 AA;
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Q95N02;
28-FEB-2003 (
28-FEB-2003 (
25-OCT-2004 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                          | XLQTMANYIALVVGCLLPPFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIF 240
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241 LLCFLPYHALRTHLVTWDADSCMDELHKATVITLTLAAANSCFNPFLYYFAGENFKARL 300
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
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    4 (Potential).

S. (Potential).

(Ytoplasmic (Potential).

( Potential).

Extracellular (Potential).

T. (Potential).

Cytoplasmic (Potential).

Cytoplasmic (Potential).

By similarity.

N-linked (GlCNRc. .) (Potential).

N-linked (GlCNRc. .) (Potential).

N-linked (GlCNRc. .) (Potential).
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                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                     69.3%; Score 1187; DB 1; Length 309; 73.1%; Pred. No. 2.3e-66;
                                                                                                                                                                                                                                   57; Indels
                                                                                                                                                                         A122AC8177879D56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
25-0CT-3004 (Rel. 45, Last annotation update)
Name-Cyslir; Synonyms-Cysli;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                339 AA
                                                                                                                                                                                                                                   26; Mismatches
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95
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166
167
309 AA;
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225; Conserv
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             DOMAIN
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TRANSMEM
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DISULFID
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CARBOHYD
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Gaps

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132 VONINLITHKKAKIVCIAIWIFVILTSSPFLMSTSYKDEKNNTKCFEPPOXNQAKYHVLV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=129/Sv;
PubMed=11226226; DOI=10.1073/pnas.041624388;
Maekawa A., Kanaoka Y., Lam B.K., Austen K.F.;
"Identification in mice of two isoforms of the cysteinyl leukotriene 1 receptor that result from alternative splicing.";
Proc. Natl. Acad. Sci. U.S.A. 98:2256-2261(2001).
                                       MNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCF
                                                               245 LPYHTLRTVHLTTWKVGLCKD-----RLHKALVITLALAAANACFNPLLYYFAGENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=CSTBL6; TISOSUE=Trachea;
MEDLINE-21562332; PubMed=11705452; DOL=10.1016/S0006-2952(01)00774-2;
Martin V., Sawyer N., Stocco R., Unett D., Lerner M.R., Abramovitz M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=CZECH II; TISSUE=Mammary gland;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Dequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21240338; PubMed=11342226; DOI=10.1016/S0167-4781(00)00271-2; Mollerup J., Jorgensen S.T., Hougaard C., Hoffmann E.K.; "Identification of a murine oysteinyl leukotriene receptor by expression in Xenopus laevis oocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                              D4
                                                                                                                                                                                                                                                                                                                                                                         099JA4; Q9JJ71; Q9JK47;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Cysteinyl leukotriene receptor 1 (CysLTR1) (Cysteinyl leukotriene receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning and functional characterization of murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=T-cell;
Ogasawara H., Izumi T., Shimizu T.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cysteinyl-leukotriene 1 (CysLT1) receptors.";
Biochem. Pharmacol. 62:1193-1200(2001).
                                                                                                                                                                                                                                                                                                                                                       352 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression in Xenopus laevis oocytes.";
Biochim. Biophys. Acta 1517:455-459(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Cysltr1; Synonyms=Cyslt1, Cyslt1r;
Mus musculus (Mouse).
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                                                                                                                                                                                                         297 KDRLKSALRK 306
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                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 DLLCVCTLPLRVVYYVHKGIWLFGDFLCRLSTYALYVNLYCSIFFWTAMSFFRCIAIVFP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 FRLLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--LQT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAIS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 ASSNTCNDTIDDFRNQVYSTLYSMITVVGFFGNGFVLYVLIKTYHEKSAYQVYMINLAVA 71
                                                                                                                                                                                                  SÜBCELLULÄR LOCATION: Integral membrane protein. SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                            Takasaki J., Kamohara M., Saito T., Matsumoto M., Matsumoto S.,
Ohishi T., Soga T., Matsushime H., Furuichi K.;
"Characterization of cloned rat and porcine cysteinyl leukotriene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Potential). (Potential). (Potential).
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PRINTS; PR01533; CYSLTRECPTR.

PRINTS; PR00237; GPCRHUDODPSN.

PROSTIE; PS00237; GROTELIN_RECEP_F1_1; FALSE_NEG.

PROSTIE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Glycoprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Extracellular (Potential).
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Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential).
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Extracellular (Potential).
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Cytoplasmic (Potential).
6 (Potential).
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Cytoplasmic (Potential)
             Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Sulna; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-linked (GlCNAc. . .)
N-linked (GlCNAc. . .)
N-linked (GlCNAc. . .)
N-linked (GlCNAc. . .)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AB052686, BAB60826.1, -.
InterPro, IPR004071; Cysleuk_receptor.
InterPro, IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 N.
38986 MW;
Name=CYSLTR1; Synonyms=CYSLT1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 37.4 es 116; Conservative
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                                                                                                                    SEQUENCE FROM N.A.
                                                                            NCBI_TaxID=9823;
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CLT1 HUMAN
AC 09Y271;
DT 28-FEB-DT 28-FEB-DT 28-FEB-DT 28-FEB-DT 28-FEB-DT 28-FEB-DT 28-FEB-DT 28-FEB-DT 28-FEB-DT 28-OCT-DE COC Butter 20 CC Butter 20 
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Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=2; Synonymas=Short; Interpretation of the property of the
                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-1- FUNCTION: Receptor for cysteinyl leukotrienes mediating construction of the microwascular smooth muscle during an inflammatory response. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. The rank order of affinities for the leukotrienes is LTD4.

-1- SUBCELLULAR LOCATION: Integral membrane protein.
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EMBL; AP329272; AAX16715.1; -
EMBL; AP26830; AAX16715.1; -
EMBL; AP26330; AAX1633.1; -
EMBL; AP26330; AAX15433.1; -
EMBL; AB044087; BAA96809.1; -
EMBL; BC027102; AAX27102.1; -
EMBL; BC0004974; F:Lelukotriene receptor activity; IDA.
GO; GO:000716; P:Cell surface receptor linked signal tran
InterPro; IPR004071; Cygleuk_receptor.
InterPro; IPR00017; Cygleuk_receptor.
Fram; PF00001; 7tm 1; Tm 1; FR00501; 7tm 1; Tm 1; FR00501; 7tm 1; EMBLYS; FR00533; GYERRHOODSN.
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Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential)
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4 (Potential).
Extracellular (Potential)
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6 (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=Long;
IsoId=Q99JA4-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Potential).
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247 YHTLRTVHLTTW--KVGLCKD--RLHKALVITLALAAANACFNPLLYYPAGENFKDRLKS 302  
264 YHIQRTIHLHLLHSETRPCDSVLRMQKSVVITLSLAASNCCFDPLLYFFSGGNFRRL-S 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 LFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPFR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 NINLVTQKKARFVCIGIWIFVILTSSPFLMYKSYQDEKONTKCFEPPQNNQAKKYVLILH 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 NNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDL
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                                                                                                                                                                                                                                                                                                                                                                                                           10; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
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28-FEB-2003 (Rel. 41, Last sequence update)
25-GCT-2004 (Rel. 45, Last annotation update)
Cysteinyl leukotriene receptor 1 (CysLJR1) (Cysteinyl leukotriene receptor) (HD4 receptor) (HG55) (HMTWF81).
Name-CYSLTR1; Synonyms-CYSLT1;
HOMO sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                (Potential). (Potential). (Potential).
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MEDLINE=99393629; PubMed=10462554;
Sarau H.M., Ames R.S., Chambers J., Ellis C., Elshourbagy N.,
                                                                                                                                                                                                                                                                                                                                                     Length 352;
                                                                                                                                                                                                                                                                                                                                                     32.7%; Score 560; DB 1; Length 35
38.5%; Pred. No. 2.38-27;
ive 69; Mismatches 108; Indele
Extracellular (Potential).
                                                                                                                                                                                                                                                                                               SBDC94B3F1CD0CAB CRC64;
                      Cytoplasmic (Potential).
Cytoplasmic (Potential).
By similarity.
N-linked (GLONAC. . .) (FN-linked (GLONAC. . . ) (F
                                                                                                   N-linked (GlCNAC. .) (
N-linked (GlCNAC. .) (
N-linked (GlCNAC. .) (
N-linked (GlCNAC. .) (
Missing (in isoform 2) /
FTId=VSP 001921.
Y -> D (in Ref. 3).
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                                                                                                                                                                                                                                                                                                        40715 MW;
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                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 38.5
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
  291
312
352
352
188
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Gequenced by the Guthrie CDNA resource center (www.cdna.org)...;
Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.

-!-FUNCTION: Receptor for cysteinyl leukortiense mediating
bronchoconstriction of individuals with and without asthma.

Stimulation by LTD4 results in the contraction and proliferation of smooth muscle, edema, eosinophil migration and damage to the mucus layer in the lung. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. The rank order of affinities for the leukotrienes is LTD4

>> LTE4 = LTC4 >> LTB4.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- SUBCELLULAR LOCATION: Midely expressed, with highest levels in spleen and peripheral blood leukocytes. Lower expression in several tissues, such as lung (mostly in smooth muscle bundles and alveolar macrophages), placenta, small intestine, pancreas, colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 300201; -. Goods of the state of the st
Foley J.J., Schmidt D.B., Muccitelli R.M., Jenkins O., Murdock P.R., Herrity N.C., Halsey W., Sathe G., Muir A.I., Nuthulaganti P., Dytko G.M., Buckley P.T., Wilson S., Bergema D.J., Hay D.W.P.; "Identification, molecular cloning, expression, and characterization of a cysteinyl leukotriene receptor."; Mol. Pharmacol. 56:657-663(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANDOUS: Selective antagonists, such as montelukast (Singulair), zafirlukast (Accolate) and pranlukast (Onon), are used in the treatment of the asthma crisis.
SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                         Warren C.N., Aronstam R.S., Sharma S.V.; "cDNA clones of human proteins involved in signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR0002/0; .....

Pfam. PP00001; 7tm_1; 1.

PRINTS; PR01533; CYSLTRECPTR.

PRINTS; PR0237; GPCRHODOPSN.

PROSITE; PS0237; GPROTEIN RECEP F1 1; FALSE NEG.

PROSITE; PS50262; GPROTEIN RECEP F1_2; 1.

Gprotein coupled receptor; Glycoprotein; Transmembrane.

G. Britanellular (Potential).

1 (Potential).
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Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential)
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Extracellular (Potential)
7 (Potential).
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2 (Potential).
Extracellular (Potential)
3 (Potential).
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498
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SEQUENCE FROM N.A.
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ACTIONES-E21388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausher R.D., Collins F.S., Wagner L., Sheafer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,
Antschench L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Raha S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Halton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Raphy J., Halton E., Ketterman M., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Robes S.J., Marra M.A.,
Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                            70 LLCVCTLPLRVYYYVHKGIWLFGDFLCRLSTYALYVNLYCSIFFWTAMSFFRCIAIVFPV 129
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                                                                                                                                                                                                                                                                                                                                                                               130 QNINLVTQKKARPVCVGIWIFVILTSSPFLMAKPQKDEKNNTKCFEPPQDNQTKNHVLVL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 PYHTLRTVHLTTW--KVGLCKD--RLHKALVITLALAAANACFNPLLYYFAGENFKDRLK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248 PYHIQRTIHLHFLHNETKPCDSVLRMQKSVVITLSLAASNCCFDPLLYFFSGGNFRKRL- 306
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                                                                                                                                                                                                                                                                                        69 LLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPF
                                                                                                                                                                                                                                                                                                                                                                                                                                  186 NYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 NSRNC--TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISD
                                                                                                                                                                                 Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                               (GlCNAc. .) (Potential)
(GlCNAc. .) (Potential)
(GlCNAc. .) (Potential)
(GlCNAc. .) (Potential)
                                                                                                                                                                             12;
                                                                                                                                            Length 337;
                                                                                                                                                                             71; Mismatches 106; Indels
                                                                                                          B9B53940F895F245 CRC64;
Cytoplasmic (Potential).
By similarity.
N-linked (GlcNAc. . .) (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-UNN-2003 (TrEMBLrel. 24, Last annotation update) Cysteinyl leukotriene receptor 1. Name=CYSLTR1; Homo sapiens (Human).
                                                                                                                                            Score 559; DB 1;
Pred. No. 2.6e-27;
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N-linked
N-linked
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                                                                                                          38541 MW;
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38.0%;
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 337
173
169
169
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262.
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CARBOHYD
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Best Local
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Q8IV19;
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7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINB=21458557; PubMed=11574155; DOI=10.1016/S0378-1119(01)00651-5;
Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,
Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
"Discovery and mapping of ten novel G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 NSRNC--TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                      Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, BC035750; AAH35750.1; -.

EMBL, BC035750; AAH35750.1; -.

GO; GO:001604974; F:leukotriene receptor activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:000786; P:G-protein coupled receptor protein signalin.

InterPro; IPR004071; Cysleuk receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                           12;
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10-0CT-2003 (Rel. 42, Lest sequence update)
11-0CT-2004 (Rel. 42, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Probable G protein-coupled receptor GPR80 (P2Y-like nucleotide receptor) (P2Y-11ke GPCR).
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                       Length 337;
                                                                                                                                                                                                                                                                                                                                                                                   32.3%; Score 553; DB 2; Length 33 37.7%; Pred. No. 6.2e-27; ive 71; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                              337 AA; 38485 MW; B9B09CE0FD305245 CRC64;
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             337 AA
                                                                                                                                                                                                                                                                                                          PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                  PRINTS; PR01533; CYSLTRECPTR. PRINTS; PR00237; GPCRRHODOPSN
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                                                                      Strausberg R.;
Submitted (JUL-2002)
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                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                               Pfam; PF00001; 7tm
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                                    SECUENCE FROM N.A.
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                                                        FISSUE=Pancreas;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                             Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S., Tsutsumi S., Aburatani H., Asai K., Akiyama Y.; "Genome-wide discovery and analysis of human seven transmembrane helix
                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=22040266; PubMed=12044878; DOI=10.1016/S0014-5793(02)02775-8;
Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
"Identification of G protein-coupled receptor genes from the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Thyroid;
Bruess M., Bonisch H., von Kugelgen I.;
"Molecular cloning and functional characterization of a new human P2Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- FUNCTION: Orphan receptor.
-i- SUBCELIULAR LOCATION: Integral membrane protein.
-i- TISSUE SPECIFICITY: Detected in kidney and, to a lower extend, i placenta. Not detected in brain tissues including the frontal cortex, caudate putamen, thalamus, hypothalamus, hippocampus or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the G-protein coupled receptor 1 family
                                                                       nek
Wittenberger T., Hellebrand S., Munck A., Kreienkamp H.-J., Schaller H.C., Hampe W.; "GRPS9, a new G protein-coupled receptor with homology to a subgroup of nucleotide receptors."; BMC Genomics 3:17-17(2002).
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PROSITE; PS00237; GFCRRHODDPSN.
PROSITE; PS00237; GFRTHODDPSN.
PROSITE; PS00237; GFRTHODDPSN.
PROSITE; PS00262; GFROTEIN_RECEP_T_1; Transmembrane.
G-protein coupled receptor; Glycoprofein; Transmembrane.
T TRANSMEM 35 55 1 (Potential).
T TRANSMEM 70 90 2 (Potential).
T TRANSMEM 11 137 3 (Potential).
T TRANSMEM 117 137 3 (Potential).
T TRANSMEM 117 137 3 (Potential).
T TRANSMEM 117 137 3 (Potential).
T TRANSMEM 152 172 4 (Potential).
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor genes.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
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Cytoplasmic (Potential).
6 (Potential).
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InterPro; IPR002286; P2 purnocptor.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome sequence.";
FEBS Lett. 520:97-101(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew; HGNC:4531; GPR80
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IsoId=Q13304-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leukoc. Biol. 59:18-23(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 2)
                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
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SAVR 318
                                                                                                                                                                                                                                                                                                                  302 SALR 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity)
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                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
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                                                                                                                                                                                                                                                               129 RLLHVTSIRSAWILCGIIWILIMASSI----MLLDSGSEQNGS----VTSCLELNLYKIAK 181
                                                                                                                                                                                                                                                                               140 SCFSIHKTRCAVVACAVVWIISLVAVIPMTFLITSTNRTNRSACLDLTSSDELNTIK--- 196
                                                                                                                                                                                                                                                                                                                182 LQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFF 241
                                                                                                                                                                                                                                                                                                                                        --WYNLILTATTFCLPLVIVTLCÝTTIIHTLTHGLQTDSCLK---QKARRLTILLLLAFY 251
                                                                                                                                                                                                                                                                                                                                                               LCFLPYHTLRTVHLTTWKVGL---CKDRLHKALVITLALAAANACFNPLLYYFAGENFKD 298
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                                                                                                                                                                             23 NCTDENIPLKMHYLPVIYGIIFLVGFPGNAVVISTYIFKMRPWKSST---IIMLNLACTD
                                                                                                                                                             14 NCTIEN--FKREFFPIVYLIFFWGVLGNG--LSIYVF-LQPYKKSTSVNVFMLNLAISD
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Sprague-Dawley;
X Pubmed-15001573; DOI-10.1074/jbc.M400360200;
X Inbe H., Watanabe S. Miyawaki M., Tanabe E., Encinas J.A.;
Inbe H., Watanabe S. Miyawaki M., Tanabe E., Encinas J.A.;
Indentification and Characterization of a Cell-Surface Receptor,
P2Y15, for AMP and Adenosine.";
I. J. Biol. Chem. 279:19790-19799(2004).
EMBL; AY191367; AAp32736.1; -
R GO; GO:0004872; Fibringral to membrane; IEA.
GO; GO:0004872; Fibringral to membrane; IEA.
GO; GO:0004872; Fireceptor activity; IEA.
GO; GO:0004872; Fireceptor activity; IEA.
GO; GO:0007186; Firhodopsin-like receptor activity; IEA.
GO; GO:0007186; Firhodopsin-like receptor protein signalin. .;
R InterPro; IPR000276; GPCR_Rhodopsin.
R InterPro; IPR000276; GPCR_Rhodopsin.
R InterPro; JPR000276; GPCR_Rhodopsin.
             (Potential).
(Potential).
(Potential).
(Potential).
                                                                                                                                      29;
                                                                                                             28.5%; Score 487.5; DB 1; Length 337; 34.9%; Pred. No. 7.3e-23; ive 64; Mismatches 114; Indels 29.
                                                                                       6814EA0044756CE6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
G protein-coupled receptor 80.
By similarity.
N-linked (GlCNAc.)
N-linked (GlCNAc.)
N-linked (GlCNAc.)
N-linked (GlCNAc.)
F - L (in Ref. 5)
K -> R (in Ref. 5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                 312 AVCSTVRCKVSGNLEQAK 329
                                                                                                                                                                                                                                                                                                                                                                                                                  RLKSALR---KGHPQKAK 313
                                                                                       38251 MW;
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PRINTS; PR01157; P2YPURNOCPTR.
                                                                                                                         Best Local Similarity 34.9
Matches 111; Conservative
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 183
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SEQUENCE
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CARBOHYD
CONFLICT
CONFLICT
SEQUENCE
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           CARBOHYD
CARBOHYD
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                80 LLYLTSLPFLIHYYASGENWIFGDFMCKFIRFGFHFNLYSSILFLTCFSLFRYIVIHPM 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 LPYHTLRTVHLTTWKVGL---CKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRLK 301
                                                                                                                                                              68
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                                                                                                                                                                                                                                   23 NCTDEQISFKMQYLPVIYSIIFLVGFPGNTVAISIYVFKMRPWKSST---IIMLNLALTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 YNLILTATTFCLPLLIVTLCYTTIISTLTHGPRTHSCFK---QKARRLTILLLLUVFYVCF
                                                                                                                                                          14 NCTIE--NFKREFFPIVYLIIFFWGVLGN--GLSIYVF-LOPYKKSTSVNVFMLNLAISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 MNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIFFLCF
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"New members of the chemokine receptor gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expressed in the
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                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                 20;
    Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                013304; OgUDZ6; QGUE21;
01-NOV-1997 (Rel. 35, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Probable P2Y purinoceptor GPR17 (P2Y-like receptor) (R12)
Query Match 28.0%; Score 479; DB 2; Length 33
Best Local Similarity 34.2%; Pred. No. 2.4e-22;
Matches 104; Conservative 66; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Hippocampus;
MEDLINE-98181695; PubMed-9523551;
Blaesius R.H., Weber R.G., Lichter P., Ogilvie A.;
Blaesius R.H., Weber R.G., Lichter P., Ogilvie A.;
"A novel orphan G protein-coupled receptor primarily exbrain is localized on human chromosomal band 2q21.";
J. Neurochem. 70:1357-1365(1998).
-:- FUNCTION: Putative receptor for purines coupled to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSLATAEQCGQETPLENMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMHLA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 HPVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQ--LYR-EKASH 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 HALVSLAVAFTFPFITTVTCYLLIIRSL-----RQGLRVEKRLKTKAVRMIAIVLAIFL 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HPFRLLHVTSIRSAWILCGIIWILI-MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQT 184
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is in no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                By similarity.
N-linked (GloNAc. ..) (Potential).
N-linked (GloNAc. ..) (Potential).
N-linked (GloNAc. ..) (Potential).
                                                                                                                                                                 GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004950; F:chemokine receptor activity; TAS.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
InterPro; IPR002786; GPCR Rhodpsn.
InterPro; IPR002286; P2_purnocptor.
                                                                                                                                                                                                                                              PRINTS, PRO0237; GPCRRHODOPSN.
PROSITE, PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
Alternative splicing; G-protein coupled receptor; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 479; DB 1; Length 367; Pred. No. 2.6e-22;
institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Pred. No. 2.6e-22;
62; Mismatches 126; Indels
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Cytoplasmic (Potential).
6 (Potential).
Extracellular (Potential).
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5 (Potential).
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132FBE97BE83C60C CRC64;
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2 (Potential).
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Missing (in isoform 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40989 MW;
                                                             EMBL; U33447; AAB16746.1; -. EMBL; Y12546; CAA73144.1; -.
                                                                           EMBL; Y12546; CAA73144.1; -. EMBL; Z94154; CAB08107.1; -. EMBL; Z94155; CAB08108.1; -. HSSP; P34996; 1DDD.
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34.8%;
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nes 112; Conservative
                                                                                                                            Genew; HGNC:4471; GPR17.
H-InvDB; HIX0002439; -
                                                                                                                                                                                                                                    Pfam; PF00001; 7tm 1; 1
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Trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Miller S.L., Feingold E.A., Grouse L.H., Derge J.G., Miller S.L., Feingold E.A., Grouse L.H., Derge J.G., Maluser R.D., Collins F.S., Wagner L., Schemen C.M., Scheler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., An Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F., Brangeton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., An Richards S., Morley K.C., Hale S., Garrinci P., Frange C., Nalask S.A., McZwan P.J., McKernan K.J., Malkey J.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A., Helton B., Ketreman M., Madan A., Young A.C., Shevchenko Y., Boutferd G.G., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutferd G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Ances S.J., Marra M.A., Smailus D.E., Schnerch A., Schein J.E., Schein J.E., Schnerch A., Schein J.E., Schein J.E., Schnerch A., Schein J.E.
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135 HPVKSLKLRRPLYAHLACAFLWVVAVAMAPLLVSPQTVQTNHTVVCLQ--LYR-EKASH 191
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                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC031653; AM431653.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:001584; F:integral to molectide receptor activity, G-.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001286; P:G-protein coupled receptor protein signalin.
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PRINTS, PRO1157, P2YPURNOCPTR.

PRO51TE, PS00237, G PROTEIN RECEP FI 1; UNKNOWN 1.

PRO51TE, PS00262, G PROTEIN RECEP FI 2; 1.

SEQUENCE 339 AA, 37860 MW; BB0CAFD0FC371D63 CRC64;
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                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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334 HALCNLLCGKRLKGPPPSFEGK 355
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InterPro; IPR002286; P2_purnocptor.
                                                                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA sequences.
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Best Local Similarity
Marches 112; Conserv
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Q8N5S7;
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                                                                                                                                     LCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 SCTFDEBERXILLPVSYSLVCFFGLILNSVALWMFITKMRPWKPST---VYMFHLALSDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUM-2003 (TrEMBLrel. 24, Created)
01-JUM-2003 (TrEMBLrel. 24, Last sequence update)
01-JUM-2003 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
SI:bZ46J2.9 (Novel protein similar to nucleotide receptors).
Name=pr2941; Synonyms=SI:bZ46J2.9; slc2sas;
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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EMBL; AL590151; CAD68067.1; --
EMBL; AL590151; CAD68067.1; --
ETN; EDB-GENE-030616-77; pr2y41
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0015021; F:purinergic nucleotide receptor activity, G-.
GO; GO:0001584; F:receptor activity; IEA.
GO; GO:000186; P:rhodopsin-like receptor activity; IEA.
GO; GO:000186; P:rhodopsin-like receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR0002186; P2_purnocptor.
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Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01056; P2Y4PRNOCPTR.
PRINTS; PR01157; P2YPURNOCPTR.
PROSITE; PS00237; G PROTEIN RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                       298 DRLKSAL----RKGHPQKAKTK 315
                                                                                                                                                                                                                                                                                                                                      306 HALCNLLCGKRLKGPPPSFEGK 327
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Matches
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AC Q7ZZA4
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DT 01-JUJ
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245 CFVPFHITRTLYY-AYRIFDADCKTLNIVNFSYKITRPLASVNSCLDPILYFLAGDHYRS 303

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us-09-826-791&-1, rni
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August 20, 2005, 04:45:55; Search time 213 Seconds (without alignments) 7628.276 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/RECOMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                               1202784 seqs, 818138359 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                 OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                       Sequence:
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                                                                                                                                                                                                               Title:
Perfect
                                                                                                                           Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES		
Result No.	Score	Match	Length	D3	ΩI	Description	
-	989.8	(69.7)		4	US-09-585-876-1	nce 1,	
8	145.2	}	1578	m	US-09-044-404A-1	H	
٣	145.2	14.6	1578	4	US-09-586-924-1	-1	
4	99.4	10.0	1020	4	US-09-170-496D-31	Sequence 31, Appl	
ហ	99.4	10.0	1900	4	US-09-016-434-1484	148	
9	σ	10.0	1901	Н	US-08-153-848-43	-	
7	σ	10.0	1901	m	US-09-299-843A-43	43,	
80	99.4	10.0	1901	ო	US-09-088-337B-43	43,	
6	99.4	10.0	1901	ស	PCT-US93-11153-43	43,	
10	99.4	10.0	2453	ß	PCT-US95-07180-1	1, A	
11	96.2	7.6	1020	4	US-09-170-496D-181	181	
12	92	9.3	1255	Н	US-08-097-938-3	3, A	
13	92	9.3	1255	-4	US-08-476-000-3	'n	
14	92	9.3	1255	н	US-08-472-840-3	'n	
15	92	9.3	1255	~	US-08-476-976-3	۳,	
16	92	9.3	1255	ო	US-08-474-410-3	۳,	
17	92	9.3	1255	m	US-08-486-673B-3	'n	
18	90	9.1	1224	~	US-08-742-440A-1	Ä	
19	90	9.1	1414	-	US-08-476-000-62	62,	
20	90	9.1	1414	-		62,	
21	96	9.1	1414	~	US-08-476-976-62	62,	
22	90	9.1	1414	m	US-08-474-410-62	62,	
23	90	9.1	1414	ო	US-08-486-673B-62	62,	
24	85.6	9.8	1567	ო	US-08-889-108-16	16,	
25	ď.	9.8	1567	ß	PCT-US94-10358-16	16,	
26	85.6	9.6	2706	ď	US-08-454-549-1	Sequence 1, Appli	
27	85.6	9.6	2706	m	US-08-454-552-1	ų	

Sequence 3, Appli Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	m	Sequence 1239, Ap	Sequence 1186, Ap	Sequence 1, Appli	Sequence 225, App	Sequence 1, Appli	Ξ	1,	Sequence 26, Appl	Sequence 107, App	Sequence 221, App	Sequence 1259, Ap
US-08-149-093A-3 US-08-911-245-3	US-08-553-058C-3	US-08-514-451A-3	US-09-170-331-3	US-09-510-473-3	US-09-048-916B-3	US-09-016-434-1239	US-09-023-655-1186	US-09-054-272-1	US-09-170-496D-225	US-08-676-351-1	US-09-170-496D-117	US-08-724-974A-1	US-09-364-425B-26	US-09-170-496D-107	US-09-170-496D-221	US-09-016-434-1259
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85.2 85.2	85.2	85.2	85.2	85.2	85.2	84.4	84.4	84.4	83.2	82.4	81.6	81.6	81.6	81.4	81.4	81.4
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APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Silos-Santiago, Immaculada
TITLE OF INVENTION: 43239, A No. 6586205el GPCR-Like Molecule and
TITLE OF INVENTION: Uses Thereof
FILE REPERENCE: 5800-88
CURRENT APPLICATION NUMBER: US/09/585,876
CURRENT FILING DATE: 2000-06-1
EARLIER APPLICATION NUMBER: 60/182,061
SARLIER PILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1401 .; 0 Length 1401; Indels Query Match 99.7%; Score 989.8; DB 4; Best Local Similarity 99.8%; Pred. No. 8.2e-307; Matches 991; Conservative 0; Mismatches 2; Sequence 1, Application US/09585876 Patent No. 6586205 GENERAL INFORMATION: ; NAME/KEY: CDS ; LOCATION: (197)...(1237) US-09-585-876-1 TYPE: DNA ORGANISM: Homo sapiens US-09-585-876-1 FEATURE ઠે 셤 ò 셤 ઠે 셤 ò a ò 셤 ò

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SOFTWARE: FASESEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/044,404A
FILING DATE: MARCH 19, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/944,795
FILING DATE: APRIL 22, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T.
                                                                                                                                                              GH-70001-1
                                                                                                                                           REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1578 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 51.5%;
Matches 451; Conservative
                                                                                                                                                                                                     TELEFAX: 610-270-5090
TELEX:
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                                                                                                                      ATCCTCTGTGGGATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGT
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 605 TTCCTGGCAATGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCTGG
                                                                                                      ATCCTCTGTGGGATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGT
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AN 7-TRANSMEMBRANE RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: BATHE, GARESH
APPLICANT: HALSEY, WENDY
APPLICANT: BLLIS, CATHERINE
APPLICANT: FOLEY, JAMES
APPLICANT: FOLEY, JAMES
APPLICANT: SARAU, HENRY
TITLE OF INVENTION: CDNA CLONE HHTMF8
TITLE OF INVENTION: A NOVEL HUMAN 7-7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09044404A Patent No. 6200775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER REALABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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US-09-044-404A-1
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Pred. No. 1.1e-35;
0; Mismatches 398;
7.0
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633 224 284

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APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Law, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT FRILIAG DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE PATENTION NUMBER: 294
SOFTWARE PATENTION NUMBER: SOFTWARE PATENTION DATE: 1998-10-13
LENGTH: 1020
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Patent No. 6555339
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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APPLICANT: BALLSEY, WENDY
APPLICANT: BALLSEY, WENDY
APPLICANT: BALLS, CATHERINE B.
APPLICANT: FOLEY, JAMES, ROBERT S.
APPLICANT: AREAU, HENRY M.
APPLICANT: CHAMBERS, JON
TITLE OF INVENTION: HUMAN 7-TRANSMEMBRANE RECEPTOR
TITLE OF INVENTION: HUMAN 7-TRANSMEMBRANE RECEPTOR
TITLE OF INVENTION: HUMAN 7-TRANSMEMBRANE RECEPTOR
TITLE OF INVENTION: HUMAN 7-TRANSMEMBRANE
TILE REPERENCE: GH-70001-1D1
CURRENT APPLICATION NUMBER: 08/09/586,924
PRIOR APPLICATION NUMBER: 08/044,404
PRIOR APPLICATION NUMBER: 08/044,404
PRIOR APPLICATION NUMBER: 08/044,795
PRIOR APPLICATION NUMBER: 08/044,795
NUMBER OF SEQ ID NOS: 2
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASTESO for Windows Version 3.0
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Patent No. 6506878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 99.4; DB 4; I pred. No. 6.1e-21; 0; Mismatches 341;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1484:
SEQUENCE CHARACTERISTICS:
LENGTH: 1900 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 48.8%;
Matches 339; Conservative
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Sequence 43, Application US/081
Sequent No. 575804
Patent No. 575804
SERERAL INFORMATION:
APPLICANT: Godiska, Ronald
                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                               ; LIBRARY: GENBANK
; CLONE: 992699
US-09-016-434-1484
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    218 TGGCCGTGGCCGACTTGTCGTGCGTGCTGGTCCTGCCCACCCGCCTGGTCTACCACTTCT 277
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Patent No. 6500938
CENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEREWITH
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: PALO ALTO STATE: CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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US-09-016-434-1484
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STREET: 31
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                                                                                                                                                491 AGAACGGCAGTGCTCACATCATGCTTAGAGCTGAATCTCTTATAAATTGCTAAGCTGCAGA 550
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APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6300 Sears Tower, 233 South Wacker Drive
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-UN-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 43, Application US/09299843A
; Patent No. 6107475
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REGISTRATION NUMBER: 43,213
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SEQUENCE CHARACTERISTICS:
LENGTH: 1901 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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APPLICANT: Gray, Patrick W.

PPLICANT: Schweikart, Vicki L.

TITLE OF INVENTION: NO. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bicknell, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
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                                                                                                                                                                                                                                                                                                                                                         6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REPERENCE/DOCKET NUMBER: 31794
TELECHONEI (312) 474-6498
TELECHONEI (312) 474-6448
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1901 base pairs
TYPE: nucleic acid
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STREET: 6300
CITY: Chicago
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; LOCATION:
US-08-153-848-43
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    6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
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Best Local Similarity 48.8%; Pred. No. 6.1e-21;
Matches 339; Conservative 0; Mismatches 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/086,337B
FILING DATE: 01-Jun.1998
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: No. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 701..1717
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
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                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
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LENGTH: 1901 base pairs
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INFORMATION FOR SEQ ID NO: 43:
                                                                                                                                                                             ZIP: 60606
COMPUTER READABLE FORM:
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                                         CITY: Chicago
STATE: Illinois
COUNTRY: USA
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Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                                      Length 1901;
                                                                                                                                                                                                                                                                                                             Score 99.4; DB 3; Length 19
Pred. No. 6.1e-21;
0; Mismatches 341; Indels
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US-09-088-337B-43
Sequence 43, Application US/09088337B
Patent No. 6348574
GENERAL INFORMATION
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                             10.0%;
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Best Local Similarity 48.8
Matches 339, Conservative
                                                                                                                                                                                  7171..107
                                                                                                                           ), NAME/KEY:
; LOCATION:
US-09-299-843A-43
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                                                                                           FEATURE:
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71 TITTCCCAATTGTATATCTGATAATATTTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCA 130
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                                                                                           131 TATATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTCATGCTAAATC
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GENERAL INFORMATION:
APPLICANT: LI, APPLICANT: LI, APPLICANT: LI, APPLICANT: LI, APPLICANT: RUBEN, STEVEN M
TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBEB69
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07180
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CITY: ROSELAND
STATE: NJ
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ZIP: 07068
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                                                                    CCATGAACTATATTGCCTTGGTGGTGGCTGCCTGCTGCCATTTTTCACACTCAGCATCT
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APPLICANT: Gray, Patrick W.
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE MATERIAL, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
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48.8%; Pred. No. 6.1e-21;
tive 0; Mismatches 341; Indels
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: END PC Compatible
COMPUTER: END PC Compatible
COMPUTER: END PC Compatible
COMPUTER: Bus PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
FILING DATE:
CLASSIFICATION NUMBER: US 07/977,452
PTILNG DATE: 17-NOV-1992
ATPORNEY/AGENT INPOWATION:
NAME: NOLANG, Greta B:
REGISTRATION NUMBER: 35,302
REFERENCE/POCKET NUMBER: 31794
TELEFRONE (312) 474-6300
TELEFRAM: (312) 474-6300
TELEFRAM: (312) 474-6448
TELEFRAM: (312) 474-648
TELERALS: SEQIEN NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1901 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
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Best Local Similarity 48.8
Matches 339; Conservative
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STATE: Illinois
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COCATION:
PCT-US93-11153-43
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ORGANISM: Homo sapiens
                                                                                                                                                         GENERAL INFORMATION:
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Pred. No. 7.2e-21;
0; Mismatches 341; Indels
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                    TCLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 325800-366
TELECOMMUNICATION INFORMATION:
TELEFAX: 201-994-1700
TELEFAX: 201-994-1700
TELEFAX: 201-994-1701
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2453 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 48.8%;
Matches 339; Conservative
06-JUNE-1995
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548..1564
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: LOCATION:
PCT-US95-07180-1
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APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT APPLICATION NUMBER: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
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Pred. No. 4.4e-20;
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Sequence 181, Application US/09170496D Patent No. 6555339
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Best Local Similarity 48.5%;
Matches 337; Conservative
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APPLICANT: SUNDELIN, JOHAN
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSES:
ADDRESS
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9.3%; Score 92; DB 1; Length 1255;
Best Local Similarity 54.4%; Pred. No. 1.1e-18;
Matches 185; Conservative 0; Mismatches 155; Indels
349 AGTGTTGTGCGTTTCCTGGCAATGGTTCACCCCTTTCGGC 388
                                                                                 see agrerecadaderarredercaretrergaaceeerangedee eos
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APPLICATION NUMBER: US/08/476,000 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/390,301 FILING DATE: 25-JAN-1995 ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste.
CITY: Washington
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REGISTATION NUMBER: 30,988
REFERENCE TUNDER: 2803-0006.20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08476000
Patent No. 5716789
GENERAL INFORMATION:
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TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHRACTERISTICS:
LENGTH: 1255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 ACTGGAAAACTGACCACTGTCTTCCTTCCAATTGTCTACAATTGTGTTTGTGTGGTGGGT 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGAACGTTTTCATGCTAAATCTGGCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCC 228
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54.4%; Pred. No. 1.1e-18;
tive 0; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               C140 RECEPTOR AND ITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,938
FILING DATE: 26-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURAAHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/POCKET NUMBER: 29,959
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAK: (202) 887-0763
                                                                                                                                                                                                                                                                                                                    APPLICANT: SUNDELIN, JOHAN
APPLICANT: SCARBORGUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR ANI
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington, D.C.
                                                                                                                                                                       Sequence 3, Application US/08097938
Patent No. 5629174
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 185; Conservative
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US-08-097-938-3
                                                                                      RESULT 12
US-08-097-938-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169
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APPLICANT: SUNDELIN, JOHAN
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
       326 TTGCCAAGTAACGGCATGGCCCTGTGGGTCTTTTCCGAACTAAGAAGAAGCACCCT 385
                                                                                             386 écrgreartracardeccaarcredectriegerefectecrererereareareteee 445
                                                                                                                                               229 TTCAGGGCTGACTATTATCTTAGAGGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGG 288
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                                                    169 GIGAACGITITCAIGCIAAAICIGGCCAITICAGAICICCIGIICAIAAGCACGCITCCC
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Pred. No. 1.1e-18;
0; Mismatches 155; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
APPLICATION NUMBER: US 08/390,301
FILING DATE: 25-JAN-1995
ATORNEY/AGENT INFORMATION:
NAME: ADLER: REGID G.
REGISTRATION NUMBER: 30,988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000 Pennsylvania Ave. N.W., Ste. 5500
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08476976
Patent No. 5874400
GENERAL INFORMATION:
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(202) 887-0763
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TYPE: nucleic acid
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Best Local Similarity 54.4
Matches 185; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STATE: D.C.
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LOCATION:
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COCATION:
US-08-476-976-3
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                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08472840
Patent No. 5763575
GENERAL INFORMATION:
APPLICANT: SUNDELIN, JOHAN
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
289 ATTAIGICTIATICCTIGIATGICACAIGIACAGCAGIATITAITTICCIGACCGIGCTG 348
                                                                                                           506 GIGCTIATIGGCTITITICIAIGGCAACAIGIACTGTICCATICTCTICAIGACCTGCCTC 565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.1e-18;
0; Mismatches 155; Indels
                                                                                                                                                                  AGTGTTGTGCGTTTCCTGGCAATGGTTCACCCCTTTCGGC 388
                                                                                                                                                                                                           566 Adridracadaderarredercarcergaacecearedede 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 2803-0006.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 92;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/390,301
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 54.4%;
Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202) 887-150
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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56
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Best Local Similarity
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; LOCATION:
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US-08-472-840-3
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Search completed: August 20, 2005, 07:35:01 Job time : 217 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

August 20, 2005, 04:38:00; Search time 3256 Seconds (without alignments) 11608.667 Million cell updates/sec Run on:

US-09-826-791A-1 993 1 atggaaccaaatggcacctt......gaaaggaaacaagagtataa 993 Title: Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

68479088 Total number of hits satisfying chosen parameters:

34239544 seqs, 19032134700 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Lighing first 45 summaries

EST: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

g		Description		CO959137 AGENCOURT	CD630086 56040032J	CD630084 56040024J	CD630072 56039924J	CD630089 56040096H	CD630075 56039988H		CD630069 56039916H	CO959148 AGENCOURT	CD630079 56040008H	CD630087 56040088H		CD630067 56039908H		CD630066 56039816R	CD630074 56039932J	_		CD630070 56039916J	CD630090 56040096J	CD630073 56039932H		CD630088 56040088J	CD630068 56039908J
SUMMARIES		ID		C0959137	CD630086	CD630084	CD630072	CD630089	CD630075	CD630077	CD630069	C0959148	CD630079	CD630087	CD630081	CD630067	CF147785	CD630066	CD630074	AK008997	CD630082	CD630070	CD630090	CD630073	CD630076	CD630088	CD630068
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	CP147786 AGENCOUNT BZ214361 CH230-331 CV030948 10235 Ful CA376521 654906 NC CR667452 Tetraodon
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                                                                                                         1. .758
/organism="Homo sapiens"
/mol type="mann"
/db xrel="taxon:9606"
/clone lib="FLp"
/note="Vector: pDrive Cloning Vector"
                                                                                                                                                                                                                                                    Query Match 68.0%; Score 675; DB 6; Lø
Best Local Similarity 98.9%; Pred. No. 5.4e-185;
Matches 701; Conservative 0; Mismatches 5;
                                        USA
                                      CA 94304,
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
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Catarrhini; Hominidae; Homo.
ftp://image.llnl.gov.image.rearrayed_plates/IRBF.preSV
a. Note: this is a NIH_MGC Library."
                                                                                                                                                                  GATTATTCTTTATTCCTTGTATGTCAACATGTACAGCAGTATTATTTCTGACCCGGCT
                                                                                                                                                                                                                                     GAGTGTTGTGCTGGCAATGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCAT
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1 (bases 1 to 758)

Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.

Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes

Genomics 84 (1), 205-210 (2004)
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                                                                      Length 720,
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                                                                  Score 693; DB 7;
Pred. No. 3e-190;
0; Mismatches 0;
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llarity 99.9%;
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCCTCTGTGGGATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 Argeraaarcredecearricagarcrecrerrearaaceaceerreecrreaggecreae 289
                                                                                                                                                                                                         Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 745)
Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.

Circular rapid amplification of cDNA ends for high-throughput
Genomics 84 (1), 205-210 (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATTATCTTAGAGGCTCCAATTGGATATTTGGAGACCTGGGCCTGCAGGATTATGTCTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCTTGTATGTCAACATGTACAGCAGTATTTATTTCCTGACCGTGCTGAGTGTTGTGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCCTCTGTGGGGATCATAGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 GGCTCTGAGCAGAACGGCAGTGTCACATCATGCTTAGAGCTGAATCTCTATAAAATTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGGAACCAAATGGCACCTTCAGCAATAACAACAGCAGGAACTGCACAATTGAAAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GGGTTGTCCATATATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 745
710 ATCGGGGCTGCGGGTTTCTCACAGGAAGGCACTGACCACCATCA 753
                                                                                                      linear
                                                                                                    CD630072 745 bp mRNA linee
56039924J1 FLP Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .745
| organism="Homo sapiens" | /mol_type="mRNA" | /mol_type="mRNA" | /clone lib="FLP" | /clone lib="FLP" | /note="Vector: pDrive Cloning Vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.8%; Score 663; DB 6; I
99.7%; Pred. No. 1.7e-181;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                     Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304,
Tel: 6508454102
Email: gfuelncyte.com.
Location/Qualifiers
                                                                                                                                                          CD630072.1 GI:40278338
                                                                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 99.7
Matches 685; Conservative
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CD630072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATTATCTTAGAGGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGGATTATGTCTTAT 349
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                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 762)
1 (bases I to 762)
1 (Sases I to 762)
2 (Sircular rapid amplification of cDNA ends for high-throughput Genomics 84 (1), 205-210 (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 666, DB 6, Length 762;
Pred. No. 2.38-182;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive_Cloning_Vector"
                                                                                                                                                                                             Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 67.1%;
Best Local Similarity 99.4%;
Matches 700; Conservative
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                                        sapiens
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 ATGCTAAATCTGGCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGCTGAC 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 GGGTTGTCCATATATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTC 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 73)

1 (bases 1 to 73)

2 (circular rapid amplification of cDNA ends for high-throughput Genomics 84 (1), 205-210 (2004)
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                                                                                                                                                                                                                                                                                                470 ATCCTCTGTGGGGATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGT
                                                                                                                               481 GGCTCTGAGCAGAACGGCAGTGTCACATCATGCTTAGAGCTGAATTCTCTATAAAATTGCT
                                                                                                                                                    530 GGCTCTGAGCAGAACGCCAGTGTCACATGCTTAGAGCTGAATCTCTATAAAATTGCT
                                                                                                                                                                                                                                                                               601 CICAGCATCIGITAICIGCIGATCATICGGGITCTGTIAAAAGIGGAGGICCCAGAAICG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 ATGGAACCAAATGGCACCTTCAGCAATAACAACAGGGAACTGCACAATTGAAAACTTC
                                                       421 ATCCTCTGTGGGATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGCTAAATCTGGCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTGAC
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="texon:9606"
/clone_lib="FLP"
/note="Vector: pbrive_Cloning_Vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.6%; Score 632; DB 6; Le 98.3%; Pred. No. 1.8e-172; iive 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102.
Email: gfu@incyte.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                           661 GGGCTGCGGGTTTCTCAC 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 63.6
Best Local Similarity 98.3
Matches 692; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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CD630075
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Fu,G.K.; Wang,J.T.; Yang,J.; Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput Genomics 84 (1), 205-210 (2004)
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                                  TATTATCTTAGAGGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGGATTATGTCTTAT
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                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                     726 bp mRNA lines
56040096H1 FLP Homo sapiens cDNA, mRNA sequence.
CD630089
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/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"
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3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102.
Email: gfu@incyte.com.
Location/Qualifiers
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                                                                                                                                                                 CGGGGCTGCGGGTTTCTCACAGGAAGG 685
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GGGTTGTCCATATATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTC
                                                                                                                                         649 AACTCAGCATCTGTTATCTGCTGATCCTTCGGGTTCTGTTAACAAGTGGAGGTCCCAGAA
                                                                                       181 ATGCTAAATCTGGCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTGAC
                                                                                                      ATGCTAAATCTGGCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTGAC
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56039916H1 FLP Homo sapiens cDNA, mRNA sequence.
CD630069
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            TATTATCTTAGAGGCTCCAATTGGATATTTGGAGACCTGGGCCTGCAGGATTATGTTAT 300
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                                                              TCCTTGTATGTCAACATGTACAGCAGTATTTATTTTCCTGACCGTGCTGAGTGTTGTGCGT 360
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                                                                                                                                         TTCCTGGCAATGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCTGG 469
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1 (bases 1 to 750)
1 (bases 1 to 750)
2 (circular rapid amplification of cDNA ends for high-throughput Gercular rapid amplification of cDNA ends for high-throughput Genomics 84 (1), 205-210 (2004)
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                                                                           ATCCTCTGTGGGATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGT
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larity 97.3%; Pred. No. 9.8e-169;
Conservative 0; Mismatches 13; Indels 6
                                                                                                                                                                                                                                                                                                                                                                              TCGGGGCTGCGGGTTTCTC---ACAGGAAGGCACTGACCACCAT 698
                                                                                                                                                                                                                                                                                                                                                                                           TCGGGGCTGCGGGGTTTCCTCACCAGGAAGGCACTGACCACCAT 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                               750 bp mRNA linear
5603996H1 FLP Homo sapiens CDNA, mRNA sequence.
CD630077
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3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102.
Email: gfu@incyte.com.
Location/Qualifiers
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Homo sapiens
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_tref="nERNA"
/db_tref="lataxon:9606"
/clone='IMAGE:788973"
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/clone_lib="NHH MGC_146"
/note="Vector: pcDNA3.1; Site 1: multiple; Site 2:
/note="Vector: pcDNA3.1; Site 3: multiple; Site 3: multiple; Organish Site 3: multiple; Organish Site 3: multiple; Diataxies orgical site 3: multiple; Indiage.rearrayed_plates/IRBF.preSV.dat
a. Note: this is a NIH_MGC Library."
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: IRBI7 row: f column: 03
High quality sequence stop: 602.

1. 729
Location/qualifiers
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(Dases 1 to 729)

NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (WGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Genomics

National Cancer Mammalian (NIH

Bldg. 31 RmilohO7 Bechesda, MD 20892

Email: cgapba-r@mail.nih.gov

Tissue Procurement: Guthrie CDNA Resource Center
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                            Length 673
                                                                    0; Indels
                          Score 618; DB 6; Le
Pred. No. 2.1e-168;
                                       100.0%; Pred. No.
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CO959148.1 GI:51323730
                            62.2%;
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                                           Best Local Similarity 100.
Matches 618; Conservative
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

DEFINITION

RESULT 9 CO959148 LOCUS

ACCESSION

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1 (bases 1 to 670)

S Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes

L Genomics 84 (1), 205-210 (2004)

Contact: Fu (2004)

Contact: Pu (2004)

Contact: Pu (2004)

Tel: 6508454102

Tel: 6508454102

Email: gfu@incyte.com.

Location/Qualifiers

I . 670
                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
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56040088H1 FLP Homo sapiens cDNA, mRNA sequence.
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TITLE
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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 652)
S Fu,G K., Wang,J., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Contact: Fu GK
Incyte Genomics 8 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
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   649 CTCAGCATCCTGTATCTGCTGATCATTCCGGTTCTTTAAAATTGAAAG---TCCNGAATC 705
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                                                                                                                                             652 bp mRNA linea
56040008H1 FLP Homo sapiens cDNA, mRNA sequence.
CD630079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .652
/organism="Homo sapiens"
                                    684
                                                                    706 NNGCTGCGGGTTTCACAAGAAG 729
                                  661 GGGTGCGGGTTCTCACAGGAAG
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Homo sapiens
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1 (bases 1 to 68).
1 (bases 1 to 68).
2 (croular rapid amplification of cDNA ends for high-throughput Genomics 84 (1), 205-210 (2004)
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                                                                                               410 TTCCTGGCAATGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCTGG
                                                                                                                                                                       470 ATCCTCTGTGGGGATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGT
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                       350 TCCTTGTATGTCAACATGTACAGCAGTATTTATTTCCTGACCGTGCTGAGTGTTGTGGG
                                                                           361 TTCCTGGCAATGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCTGG
                                                                                                                                                   421 ATCCTCTGTGGGATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGT
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56039908H1 FLP Homo sapiens CDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Incyte Genomics, Inc.
3160 Forter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102.
Email: gfu@incyte.com.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone lib="FLP"
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Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 663)
Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput
Genomics 84 (1), 205-210 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 ATGGAACCAAATGGCACCTTCAGCAATAACAACAGCAGGAACTGCACAATTGAAAACTTC 109
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                                 421 ATCCTCTGTGGGATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGT
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56040016H1 FLP Homo sapiens cDNA, mRNA sequence.
CD630081
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/organisme"Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3160 Porter Dr., Palo Alto, CA 94304, USA Tel: 6508454102
Email: gfu@incyte.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD630081.1 GI:40278347
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clone and include the following: 5'-EcoRV-XmnI/XhoI-3', 5'-ECoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.lanh.gov/image/rearrayed_plates/IRBI.preSV.dat a Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 12-JAN-2004
                                                                                                                                                                                                                                                                                  AAGAGAGAATTTTCCCCAATTGTATATCTGATAATATTTTTTGGGGAGTCTTGGGAAAT 120
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                                                                                                                                          Score 565; DB 7;
Pred. No. 6e-153;
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                                                                                                                                          56.9%; Score 565; DE ilarity 100.0%; Pred. No. 6e-Conservative 0; Mismatches
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3160 Porter Dr., Palo
Tel: 6508454102
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Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm.OAO7 Betheda, MD 20892
Email: cgapbs-romail.nih.gov
Tissue Procurement: GPCR Consortium
CDNA Library Preparation: GPCR Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
CDNA Library Arrayed by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://imago.lln.gov
Plate: IRBIO2 row: f column: 05
High quality sequence stop: 659.
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/clone lib="NIH MGC 145"
/clone lib="NIH MGC 145"
/clone lib="NiH MGC 145"
/clone lib="Vector: pcDN3.1; Site l: varies by clone; Site 2: varies by clone; ORF8 were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by
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     ATGCTAAATCTGGCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTGAC 289
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Email: gfu@incyte.com.
Location/Qualifiers
1. .63
/ organism="Homo sapiens"
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                                                                                                                          Query Match
54.7%; Score 543; DB 6; I
Best Local Similarity 99.8%; Pred. No. 1.5e-146;
Matches 554; Conservative 0; Mismatches 0;
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Search completed: August 20, 2005, 07:31:15 Job time : 3259 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

August 20, 2005, 02:24:45; Search time 4426 Seconds (without alignments) 10871.222 Million cell updates/sec Run on:

US-09-826-791A-1 993 1 atggaaccaaatggcacctt......gaaaggaaacaagagtataa 993 Title: Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

9416466 Total number of hits satisfying chosen parameters:

4708233 seqs, 24227607955 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

gp ba: \*
gp high a: \*
gp on: \*
gp on: \*
gp on: \*
gp pi: \*
gp pi: \*
gp ro: \*
gp ro: \*
gp ro: \*
gp ro: \*
gp vi: \* ¢enEmb}:• Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES		
Result		Query	•			-	
No.	Score	Match	Match Length DB	8	QI	Description	ion
7	993	100.0	993	9	AX304812	AX304812	Sequence
7	993	100.0	993	9	BD131273	BD131273	Novel pol
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4	993	100.0	1026	9	AX644576	AX644576	Sequence
'n	993	100.0	1041	9	BD144304	BD144304	Novel G-p
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6	993	100.0	1041	9	AX281256	AX281256	
01	993	100.0	1041	9	AX304816	AX304816	
11	993	100.0	1041	9	AX417072	AX417072	
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15	993	100.0	1041	σ	AF254664	AF254664	Homo sapi
þ	993	100.0	1041	6	AY389504	AY389504	Homo sapi
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19	993	100.0	1430	9	AX252469	AX252469	Sequence

	BC069160 Homo sapı BD188750 Peptide 1 AX549303 Sequence BD013097 Peptide 1 AB038269 Homo sapi		ABO22662 Sub BCFOI BD188765 Peptide 1 BD13112 Peptide 1 BD188768 Peptide 1 BD013115 Peptide 1 AC111418 Rattus no AR058930 Mus muscu	AC116884 Mus muscu AF331658 Mus muscu AB052661 Rattus no AY462139 Chinchill
6 AX281258 6 AX329226 6 AX319323 6 AX644523	9 BC069160 6 BD188750 6 AX549303 6 BD013097 9 AR279611	9 AL137118 6 AX211656 6 AX148246 6 AR349928 6 AX211539	4 ABUS2662 6 BD188765 6 BD013112 6 BD013115 7 AC111418	2 AC116884 10 AF331658 10 AB052661 10 AY462139
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## ALIGNMENTS

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linear	Vertebrata; i; Hominidae;	Hafland, L. Hummn-cysteniyl leukotriene receptor (cyslt2) Patent: EP 1158050-A 1 28-NOV-2001; Pfizer Limited (GB) , PPIZER INC. (US)			; Length 993; 86; 0; Indels	atggaaccaaatggcaccttcagcaataacaacagcaggaactgcacaattgaaaacttc 	AAGAGAGAATTTTTCCCAATTGTATGTGATAATATTTTTCTGGGGAGTCTTGGGAAAT	AAGAGAGAATTTTCCCAATTGTATATCTGATAATATTTTTCTGGGGAGTCTTGGGAAAT	GGGTTGTCCATATATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTC	GGGTTGTCCATATATGTTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTC	ATGCTAAATCTGGCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTGAC	ATGCTAAATCTGGCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGCTGAC
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ър 3050		ecep 7-200 INC.	ens d Di	;	ore 993; ed. No. 2. Mismatches	A = C	ČTG –	-cra	SC-I	CCT	CTG	-25
993 bp EP1158050	Chordata; Primates;	kotriene r A 1 28-NOV ; PFIZER	<pre>cocation/Qualifiers 1993 forganism="Homo sapiens" mol_type="unassigned DN db xref="taxon:9606"</pre>		Score 993; Pred. No. Mismatch		ATA	ATA	25 25 25 25 25 25 25 25 25 25 25 25 25 2	CCAC	TCTC	- Li
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from Patent GI:17644492	Homo sapiens (human Homo sapiens Bukaryota; Metazoa; Mammalia; Butheria;	Harland, L.) Human-cysteinyl leu Patent: EP 1158050- Pfizer Limited (GB)	Location/Qualifiers 1993 /organism="Homo sap/mol_type="unassign/db xref="taxon:960"		100 larity 100 Conservative	29-55 	TTI OH	LITC	ATAT	ATAT	3990	-00 -00 -00 -00 -00 -00 -00 -00 -00 -00
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	sapiens sapiens yota; Me	Light H	н п 🔍 🤍		similarity 3; Conser	AACI	GAG	GAG	TGTC	TGTO	TAAT	TA.
AX304812 Sequence AX304812 AX304812	Homo sapie Homo sapie Eukaryota Mammalia;	Harland, L Human—cyst Patent: El			.ન	ATGG	AAGA  -	AAGA	- - -	9661	ATGC	ATGC
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C1AN15-769, AGIX39/395, AGIX39/395, AGIX45/00, AGIX48/00, AGIP1/04,

AGIP1/00, AGIP11/02, AGIP11/06, AGIP19/00, AGIP29/00, AGIP31/00,

AGIP37/00,

C07X14/47, C07X16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10 PC
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PF 05-APR-2001 JP 2001106882
PR 45-APR-2000 GB 0008504:3
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PC 012A15-709, AGIX39/395, AGIX45/00, AGIX48/00, AGIP1/04, AGIP1/00, AGIP1
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Catarrhini, Hominidae, Homo.
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Patent: JP 2002017378-A 1 22-JAN-2002;
PFIZER INC
OS Homo sapiens (human)
PN JP 2002017378-A/1
PD 22-JAN-2002
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Eukaryota; Metazoa; C
Mammalia; Eutheria; P
1 (bases 1 to 993)
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1 ATGGAACCAAATGGCACCTTCAGCAATAACAACAGCAGGAACTGCACAATTGAAAACTTC
                                                                                                121 GGGTTGTCCATATATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTC
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ESGLRVSHRKALTTIIILIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLA
LAAANACFNPLLYYPAGENFKDRLKSALRKGHPQKAKTKCVFPVSVWLRKETRV"
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Homo sapiens
Homomalia; Metacas, Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 993)
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                                TTCTTGTGTTTCCTGCCCTATCACACACTGAGGACCGTCCACTTGACGACATGGAAAGTG
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Published Only in DataBase (2000)
2 (bases 1 to 993)
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Submitted (10-fAPR-2009) Hinako Suga, Faculty of Medicine,
University of Tokyo, Department of Neurochemistry, 7-3-1,
Tokyo 113-0033, Japan (E-mail:hsuga@m.u-tokyo.ac.jp,
Tel:81-3-5841-3560, Fax:81-3-3814-8154)
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cysteinyl leukotriene receptor like receptor.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Chases I to 1041)

Haga,T., Takeda,S. and Miyake,N.

Novel G-protein coupled receptors

Detent: JP 2002112793-A 29 16-APR-2002;

JAPAN SCIENCE AND TECHNOLOGY CORP

OS Homo sapiens (human)

PN JP 2002112793-A/29

PD 16-APR-2002

PP 09-FEB-2001 JP 2001034434

PI TATSUYA HAGA, SHIGEKI TAKEDA, NARIKI MIYAKE

PC CI2NIS,O9,A01K67/027,A61K38/00,A61K39/395,A61K35/00, PC
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                           CTCAGCATCTGTTATCTGCTGATCATTCGGGTTCTGTTAAAAGTGGAGGTCCCAGAATCG
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Novel G-protein coupled receptors
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100.0%; Pred. No. 3e-286;
tive 0; Mismatches 0;
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Novel G-protein coupled receptors.
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JP 2002112793-A/29.
Homo sapiens (human)
Homo sapiens
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                                                                                                                              Feder, J., Nelson, T.C., Ramanathan, C., Cacace, A.M. and Barber, L.B. A novel human g-protein coupled reciptor hgprbmyll expressed highly in heart and variants thereof Patent: WO 02086123-A 54 31-OCT-2002; Bristol-Myers Squibb Co. (US)

Location/Qualifiers
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RLHKALVITLALAAANACFNPLLYYFAGGENFKDRLKSALRKGHPQKAKTKCVFPVSVW
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                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
1. .1026
/note="unnamed protein product"
                           sapiens (human)
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                         AAGAGAGAATTTTTCCCAATTGTATATCTGATAATATTTTTTCTGGGGAGTCTTGGGAAAT
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CQ739544 1041 bp DNA Sequence 25478 from Patent WO02068579.

RESULT 6 CQ739544 LOCUS DEFINITION

ö 120 240 540 168 180 228 288 TATTATCTTAGAGGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGGATTATGTCTTAT 300 348 360 408 420 468 480 528 588 600 648 99 708 720 768 9 Homo sapiens (human) Homo sapiens Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. GGGTTGTCCATATATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTC TATTATCTTAGAGGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGGATTATGTCTTAT Trcciggcaatggttcacccctttcggcttctgcatgtcaccagcatcaggagggcctgg ATCCTCTGTGGGGATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGT CTCAGCATCTGTTATCTGCTGATCATTCGGGTTCTGTTAAAAAGTGGAGGTCCCAGAATCG 1.
Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other thereof
Patent: WO 02068579-A 25478 06-SEP 2002;
PE Corporation (NY) (US) GGGTTGTCCATATATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTC ATGCTAAATCTGGCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTGAC TICCTGGCAATGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCTGG CTCAGCATCTGTTATCTGCTGATCATTCGGGTTCTGTTAAAAGTGGAGGTCCCAGAATCG GGGCTGCGGGTTTCTCACAGGAAGGCACTGACCATCATCATCATCATCATCATCTTC GGGCTGCGGGTTTCTCACAGGAAGGCACTGACCATCATCATCATCACCTTGATCATCTTC ö Length 1041; Indels Match 100.0%; Score 993; DB 6; Local Similarity 100.0%; Pred. No. 3e-286; les 993; Conservative 0; Mismatches 0; 1. .1041
/organism="Homo sapiens"
/mol\_type="unassigned DNA"
/db\_xref="taxon:9606" 709 199 B ઠે 셤

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                    409 TTCCTGGCAATGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGAGTGCCCTGG
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Parent: WO 0168842-A 1 20-SEP-2001;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
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/db_xref="taxon:9606"
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                 TTCTTGTGTTTCCTGCCCTATCACACACTGAGGACCGTCCACTTGACGACATGGAAAGTG
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Patent: WO 0136471-A 13 25-MAY-2001;
Arena Pharmaceuticals, Inc. (US)
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 13 from Patent WO0136471.
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100.0%; Score 993; DB 6;
Best Local Similarity 100.0%; Pred. No. 3e-286;
Matches 993; Conservative 0; Mismatches 0;
                                                       Xiao,Y.
Regulation of human cyslt2-like gpcr
Patent: WO 0177149-A 1 18-007-2001;
Bayer Aktiengsellschaft (DE)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
 AX281256.1 GI:16608512
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REGENERON PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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/organism="Homo sapiens"
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Sequence 6 from Patent W00192302.
AX417072 GI:21449674
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Mammalia; Eutheria; Primates;
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/b xref="G1:1764496"

/db xref="G1:1764496"

/translation="MERKENSLOPSISVSEMEPNGTFSNNNSRNCTIENFKREFFPIV
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GLCKDRHKALVITLALAAANACFNPLLYYFAGENFKDRLKSALRKGHPQKAKTKCVF
PVSVWLRKETRV"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                               GGTTTATGCAAAGACAGACTGCATAAAGCTTTGGTTATCACACTGGCCTTTGGCAGCAGCC
                                                                                             ATGCTAAATCTGGCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTGAC
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Patent: EP 1158050-A 5 28-NOV-2001;
Pfizer Limited (GB) ; PFIZER INC. (US)
Location/Qualifiers
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    /note="unnamed protein product"

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/organism="Homo sapiens"
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/db_xref="taxon:9606"
1. .1041
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Sequence 5 from Patent EP1158050.
AX304816
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Best Local S:
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
ATGGAACCAAATGGCACCTTCAGCAATAACAACAGCAGGAACTGCACAATTGAAAACTTC
                                               AATGCCTGCTTCAATCCTCTGCTCTATTACTTTGCTGGGGAGAATTTTAAGGACAGACTA
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0; Mismatches 0;
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Sequence 29 from Patent WO02086123.
AX644551
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Yliffpemgylgnglsiyvflopfkkstsvnvfmlnlaisbllfistlefradyylrgs
NWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCG
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ICYLLIIKVLKVEVPESGLRVSHRKALTTIIITLIIPFCFLPYHTLRTVHLTTWKV
GLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRLKSALRKGHPQKAKTKCVF
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Pred. No. 3e-286;
                                               product"
                                                                                                                                                                                                                                                                                             Mismatches
 type="unassigned DNA"
                                                                               /proteIn_id="CAD35281.1"
/db_xref="GI:21449675"
                                                 /note="unnamed protein
               db_xref="taxon:9606"
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    HARLAND LEE
CIZNI5/09,A61K39/395,A61K39/395,A61K45/00,A61K48/00,A61P1/04,
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                                 A61P9/00,
A61P11/00,A61P11/02,A61P11/06,A61P19/00,A61P29/00,A61P31/00,
A61P37/00,
                                                                                                            C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, G01N33/566,
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                                                                              C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10
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100.0%; Pred. No. 3e-286;
ive 0; Mismatches 0
                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
                                                                                                                                           C12N5/00
Novel polypeptide
Key Loc
CDS (1)
 PI HARLAND LEE
PC CI2N15/09,A61K39
PC A61P9/00,
PC A61P37/00,
PC COYK14/47,COYK16
,C12N9/00,C12P21/02,
PC C12Q1/02,C12Q1/6
C12N15/00,
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Best Local Similarity 100.
Matches 993; Conservative
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Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                               CTCAGCATCTGTTATCTGCTGATCATTCGGGTTCTGTTAAAAGTGGAGGTCCCAGAATCG
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                                                                                                           TTCCTGGCAATGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCTGG
                                                                                                                                                                                         ATCCTCTGTGGGATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGT
                                                                                                                                                                                                                                                                                              GGTTTATGCAAAGACAGACATAAAGCTTTGGTTATCACACTGGCCTTGGCAGCC
                                                                 TCCTTGTATGTCAACATGTACAGCAGTATTTATTTTCCTGACCGTGCTGAGTGTTGTGT
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                                              TCCTTGTATGTCAACATGTACAGCAGTATTTATTTTCCTGACCGTGCTGAGTGT
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Patent: JP 2002017378-A 4 22-JAN-2002;
PFIZER INC
OS Homo sapiens (human)
PN JP 2002017378-A/4
PD 22-JAN-2002
PP 05-APR-2001 JP 2001106882
PR 05-APR-2000 GB 0008504:3
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JP 202017378-A/4
22-JAN-2002
05-APR-2001 JP 2001106882
05-APR-2000 GB 0008504:3
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Mammalia; Butheria; Primates;
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Homo sapiens (human)
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AF254664 10-OCT-2000 Homo sapiens cysteinyl leukotriene receptor CYSLT2 gene, complete
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                                                                      ATGGAACCAAATGGCACCTTCAGCAATAACAACAGCAGGAACTGCACAATTGAAAAACTTC
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YLIFFWGVLGNGLSIYVFLOPYKKSTSNVVPRILAISDLEISTLEPREADYYLRGS
YWLIFFWGLGAGGLSIYVFLOPYKSTSNVVPRILAINTAISDLEISTLESTRADYYLRGS
YWLIFFWGLGNENGSTYNWYSSIYFLTVLSVVRFLAWHPFRLLHTTSIRSAWILCG
IIWILLIMASSIWLLDSGSEGNGSVTSCLELLIYKIAKLQTWNYIALVVGCLLPFFTLS
ICYLLIIRVLKVEVPESGLRVSHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKV
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Identification of G protein-coupled receptor genes from the
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/protein_id="BAB89316.1"
/db_xref="G1:20152270"
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                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="hGPCR21"
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ICYLLIRVLKVVEVPESGLRVSHRKALTTIIITLIIPFLCFLPYHTLRTVHLTTWKV
GLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRLKSALRKGHPQKAKTKCVF
PVSVWLRKETRV"
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Direct Submission
Submitted (11-APR-2000) Pharmacology, Univeristy of Virginia School
of Medicine, 1300 Jefferson Park Avenue, Charlottesville, VA 22908,
USA
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                                                                                                                      Eukaryott; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1041)
1 Heise, C. E., O'bowd, B.F., Figueroa, D.J., Sawyer, N., Nguyen, T., Im, D.S., Stocco, R., Bellefeuille, J.N., Abramovitz, M., Cheng, R., Williams, D.L. Jr., Zeng, Z., Liu, Q., Ma, L., Clements, M.K., Coulombe, N., Liu, Y., Austin, C.P., George, S.R., O'Neill, G.P., Metters, K.M., Lynch, K.R. and Evans, J.F.
Characterization of the human cysteinyl leukotriene 2 receptor J. Biol. Chem. 275 (39), 30531-30536 (2000)
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/product="cysteinyl leukotriene receptor CYSLT2"
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    1041
    /organism="Homo sapiens"
/mol_type="genomic DNA"
    /db_xref="taxon:9606"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229
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